

*check hit 10  
mur leu 3a*

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 13.5484 Seconds  
(without alignments)  
49.176 Million cell updates/sec

Title: US-09-701-001b-1  
Perfect score: 27  
Sequence: 1 DYVIN 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database:

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| 10: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA1989.DAT:* |
| 11: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA1990.DAT:* |
| 12: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA1991.DAT:* |
| 13: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA1992.DAT:* |
| 14: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA1993.DAT:* |
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| 19: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA1998.DAT:* |
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| 21: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA2000.DAT:* |
| 22: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT:* |
| 23: | /SID2/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 27    | 100.0       | 5      | 21 | AAV59256 | Antibody 4H5 H cha |
| 2          | 27    | 100.0       | 5      | 21 | AAV51133 | Murine CD4/CD3 re  |
| 3          | 27    | 100.0       | 61     | 23 | ABP07152 | Human ORFX protein |
| 4          | 27    | 100.0       | 110    | 21 | AAV59262 | Antibody 4H5 H cha |
| 5          | 27    | 100.0       | 110    | 21 | AAV51139 | Murine derived pro |
| 6          | 27    | 100.0       | 113    | 22 | ABP71922 | Drosophila melanog |
| 7          | 27    | 100.0       | 118    | 21 | AAV59266 | Antibody 4H5 H cha |
| 8          | 27    | 100.0       | 118    | 21 | AAV51143 | Murine derived pro |
| 9          | 27    | 100.0       | 118    | 21 | AAV51145 | Murine derived pro |
| 10         | 27    | 100.0       | 122    | 11 | AAV04135 | Anti-Leu 3a heavy  |

|    |    |       |     |    |           |
|----|----|-------|-----|----|-----------|
| 11 | 27 | 100.0 | 131 | 22 | AAV64639  |
| 12 | 27 | 100.0 | 136 | 11 | AAV04133  |
| 13 | 27 | 100.0 | 149 | 22 | ABP68170  |
| 14 | 27 | 100.0 | 303 | 23 | ABP54572  |
| 15 | 27 | 100.0 | 305 | 21 | AAV59264  |
| 16 | 27 | 100.0 | 305 | 21 | AAV59265  |
| 17 | 27 | 100.0 | 305 | 21 | AAV51141  |
| 18 | 27 | 100.0 | 305 | 21 | AAV51142  |
| 19 | 27 | 100.0 | 348 | 21 | AAV82330  |
| 20 | 27 | 100.0 | 348 | 21 | AAV6816   |
| 21 | 27 | 100.0 | 366 | 18 | AAV40248  |
| 22 | 27 | 100.0 | 399 | 21 | AAV43940  |
| 23 | 27 | 100.0 | 444 | 23 | ABP29082  |
| 24 | 27 | 100.0 | 507 | 22 | AAV34756  |
| 25 | 27 | 100.0 | 543 | 22 | ABP63767  |
| 26 | 27 | 100.0 | 616 | 22 | ABP60600  |
| 27 | 27 | 100.0 | 722 | 22 | ABP52638  |
| 28 | 27 | 100.0 | 778 | 22 | ABP59200  |
| 29 | 27 | 100.0 | 933 | 19 | AAV98599  |
| 30 | 27 | 100.0 | 990 | 23 | ABP09640  |
| 31 | 26 | 96.3  | 97  | 22 | AAV03560  |
| 32 | 26 | 96.3  | 99  | 23 | ABP04400  |
| 33 | 26 | 96.3  | 102 | 22 | AAV03006  |
| 34 | 26 | 96.3  | 113 | 20 | AAV04864  |
| 35 | 26 | 96.3  | 122 | 21 | AAV56333  |
| 36 | 26 | 96.3  | 127 | 20 | AAV04862  |
| 37 | 26 | 96.3  | 139 | 22 | AAV35109  |
| 38 | 26 | 96.3  | 146 | 21 | AAV56333  |
| 39 | 26 | 96.3  | 157 | 21 | AAV55873  |
| 40 | 26 | 96.3  | 182 | 22 | AAV82660  |
| 41 | 26 | 96.3  | 214 | 21 | AAV807844 |
| 42 | 26 | 96.3  | 215 | 21 | AAV807844 |
| 43 | 26 | 96.3  | 223 | 22 | AAV08083  |
| 44 | 26 | 96.3  | 233 | 23 | ABP39000  |
| 45 | 26 | 96.3  | 249 | 21 | AAV41705  |

ALIGNMENTS

RESULT 1  
AAV59256  
AAV59256 standard; peptide: 5 AA.  
ID  
AC AAV59256;  
XX  
DT 17-APR-2000 (first entry)  
XX  
DE Antibody 4H5 H chain variable region CDR1 fragment.  
XX  
XX CD4 antigen; anti-human; antibody; 4H5; drug; CDR;  
KW complementarity determining region.  
KW  
XX  
OS Mus sp.  
XX  
XX JP11332563-A.  
XX  
XX 07-DEC-1999.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX (ASAH ) ASAH KASEI KOGYO KK.  
XX  
XX WPI: 2000-091351/08.  
XX  
XX An antibody and the nucleic acid coding the antibody -  
XX  
XX Claim 1; Page 14; 25pp; Japanese.  
XX  
XX The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC

CC application for drugs. It is highly safe in human dose. Sequences  
 CC AAY59256-58 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the H chain variable region of the  
 CC antibody 4H5 respectively.  
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 27; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIN 5  
 |||||  
 DB 1 DYVIN 5

RESULT 2  
 AAY51133  
 ID AAY51133 standard; Protein; 5 AA.  
 XX  
 XX AAY51133;

31-MAR-2000 (first entry)

DE Murine CD4/CD34 recognizing antibody heavy chain CDR-1 region #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; complementarity determining region;  
 KW CDR-1; heavy chain; murine.

OS Mus sp.

W09961629-A1

02-DEC-1999.

24-MAY-1999; 99MO-JP02711.

25-MAY-1998; 98JP-0159957.

PR 26-MAY-1998; 98JP-0163023.

PA (ASAH ) ASAMI KASEI KOGYO KK.  
 PA (ASAH ) ASAMI MEDICAL CO LTD.

PI Ono M, Soka T, Morimoto I, Miyamura K;

WPI; 2000-086720/07.

DR Devices containing antibodies recognising CD4 or CD34 and their use for  
 XX the separation of CD4 or CD34 positive cells -  
 XX

PS Claim 3; Page 75; 11pp; Japanese.

CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived complementarity determining  
 CC region CDR-1 protein fragment which is used to illustrate the method of  
 CC the invention.

Sequence 5 AA;

Query Match 100.0%; Score 27; DB 21; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIN 5

DB |||||  
 1 DYVIN 5

RESULT 3  
 ABP07152  
 ID ABP07152 standard; Protein; 61 AA.  
 XX  
 XX ABP07152;

25-JUN-2002 (first entry)

DE Human ORFX protein sequence SEQ ID NO:14286.

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.

OS Homo sapiens.

W0200192523-A2.

06-DEC-2001.

29-MAY-2001; 2001WO-US10836.

30-MAY-2000; 2000US-206132P.

PR 29-AUG-2000; 2000US-228716P.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach MD;

WPI; 2002-106308/14.

DR N-PSDB; ABN22904.

PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders -  
 XX  
 XX Disclosure; SEQ ID 14286; 1037pp; English.

CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

us-09-701-001b-1.l.rag

Fri Feb 14 15:00:47 2003

SQ Sequence 61 AA;  
 Query Match 100.0%; Score 27; DB 23; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYVIN 5  
 DB 24 DYVIN 28  
 RESULT 4  
 AAY59262  
 ID AAY59262 standard; protein; 110 AA.  
 XX  
 AC AAY59262;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 DT Antibody 4H5 H chain variable region.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 XX  
 DR N-PSDB; AAZ58661.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 XX  
 PS Claim 5; Page 15; 25pp; Japanese.  
 XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain variable region of the antibody 4H5.  
 CC  
 Sequence 110 AA;  
 Query Match 100.0%; Score 27; DB 21; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYVIN 5  
 DB 23 DYVIN 27  
 RESULT 5  
 AAY51139  
 ID AAY51139 standard; protein; 110 AA.  
 XX  
 AC AAY51139;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 DE Murine derived protein fragment #1.  
 XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX  
 OS Mus sp.

XX WO9961629-A1.  
 PN  
 XX 02-DEC-1999.  
 PD  
 XX 24-MAY-1999; 99WO-JP02711. *int pat purg*  
 PF  
 XX 25-MAY-1998; 98JP-0159957.  
 PR  
 XX 26-MAY-1998; 98JP-0163023.  
 PR  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX  
 DR WPI; 2000-086720/07.  
 DR N-PSDB; AAZ44203.  
 XX  
 PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 PS Claim 22; Page 78; 111pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 SQ Sequence 110 AA;  
 Query Match 100.0%; Score 27; DB 21; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYVIN 5  
 DB 23 DYVIN 27  
 RESULT 6  
 ABB71922  
 ID ABB71922 standard; protein; 113 AA.  
 XX  
 AC ABB71922;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 42558.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX

DR WPI; 2001-656860/75.  
 XX N-PSDB; ABL16025.  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 42558; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

Sequence 113 AA;

Query Match 100.0%; Score 27; DB 22; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 |||||  
 Db 54 DYVIN 58

RESULT 7  
 AAY59266  
 ID AAY59266 standard; protein; 118 AA.  
 XX  
 AC AAY59266;

17-APR-2000 (first entry)  
 Antibody 4H5 H chain fragment.  
 DE  
 XX  
 XX CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX

Mus sp.  
 XX  
 XX JP11332563-A.  
 XX  
 XX  
 PD 07-DEC-1999.

26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX

(ASAH ) ASahi KASEI KOGYO KK.  
 XX  
 PA WPI; 2000-091351/08.  
 DR N-PSDB; AAY58689.  
 XX

An antibody and the nucleic acid coding the antibody -  
 PS Disclosure; Page 22; 25pp; Japanese.  
 XX

CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents a H chain fragment of the antibody 4H5.  
 XX

Sequence 118 AA;

Query Match 100.0%; Score 27; DB 21; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 |||||  
 Db 31 DYVIN 35

RESULT 8  
 AAY51143  
 ID AAY51143 standard; Protein; 118 AA.  
 XX  
 AC AAY51143;

31-MAR-2000 (first entry)

XX Murine derived protein fragment #5.  
 DE  
 XX

KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX

OS Mus sp.  
 XX

PN WO9961629-A1.  
 XX

PD 02-DEC-1999.  
 XX

PF 24-MAY-1999; 99WO-JP02711.  
 XX

PR 25-MAY-1998; 98JP-0159957.  
 XX

PR 26-MAY-1998; 98JP-0163023.  
 XX

PA (ASAH ) ASahi KASEI KOGYO KK.  
 PA (ASAH ) ASahi MEDICAL CO LTD.  
 XX

PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX

WPI; 2000-086720/07.  
 XX

Devices containing antibodies recognising CD4 or CD34 and their use for  
 the separation of CD4 or CD34 positive cells -  
 XX

PS Disclosure; Page 94-95; 111pp; Japanese.  
 XX

CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX

SQ Sequence 118 AA;

Query Match 100.0%; Score 27; DB 21; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 |||||  
 Db 31 DYVIN 35

RESULT 9  
 AAY51145

ID AAY51145 standard; Protein; 118 AA.  
 XX

AC AAY51145;

DT 31-MAR-2000 (first entry)  
 XX

*just put puny*



us-09-701-001b-1.rag

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DE Murine derived protein fragment #7.  
XX Cluster differentiation: cell separation; antibody; CD4; CD34; leukemia;  
XX hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.  
XX Mus sp.  
XX WO9961629-A1.  
XX 02-DEC-1999.  
XX 24-MAY-1999; 99WO-JP02711.  
XX 25-MAY-1998; 98JP-0159957.  
XX 26-MAY-1998; 98JP-0163023.  
XX (ASAH) ASAHI KASEI KOGYO KK.  
XX (ASAH) ASAHI MEDICAL CO LTD.  
XX Ono M, Soka T, Morimoto I, Miyamura K;  
XX WPI; 2000-086720/07.  
XX N-PSDB; AA24231.  
XX Devices containing antibodies recognising CD4 or CD34 and their use for  
XX the separation of CD4 or CD34 positive cells -  
XX Disclosure; Page 96-97; 11pp; Japanese.  
XX This invention describes a novel device (I) for separating cluster  
XX differentiation (CD)-positive cells using a recombinant (chimeric or  
XX single-chain) antibody recognising CD4 or CD34. The devices are useful  
XX for the separation of CD4 or CD34 positive cells, which is useful for  
XX the collection of hematopoietic undifferentiated cells, elimination of  
XX lymphocytes from cells to be used in bone marrow transplantation, the  
XX detection of leukemic cells and the production of medicinal  
XX compositions for the treatment of HIV infection and autoimmune diseases.  
XX This sequence represents a murine derived protein fragment which is used  
XX to illustrate the method of the invention.  
XX Sequence 118 AA;  
SQ

*mut pet print*

Query Match 100.0%; Score 27; DB 21; Length 118;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DYVIN 5  
|||||  
31 DYVIN 35

RESULT 10  
AAR04135 standard; protein; 122 AA.  
ID AAR04135  
AC AAR04135;  
XX 06-SEP-1990 (first entry)  
XX Anti-Leu 3a heavy chain variable region gene product, KOL/316 Vh.  
XX HIV; AIDS; anti-Leu3A; vaccine; ds.  
XX Mus musculus.  
XX EP365209-A.  
XX 25-APR-1990.  
XX 11-OCT-1989; 89EP-0010415.  
XX 17-OCT-1988; 88US-0260558.  
XX

XX (BECT) BECTON DICKINSON CO.  
XX Hinton R, Oi VT;  
XX WPI; 1990-126329/17.  
XX N-PSDB; AAQ04042.  
XX New chimeric variants of murine antibody anti-leucine -  
XX contg. human antibody regions, and DNA encoding sequences.  
XX Claim 5; Fig 5; 12pp; English.  
XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
XX used to form chimeric mouse-variable, human-constant region Abs  
XX suggested as being useful as a vaccine to HIV.  
XX Sequence 122 AA;  
SQ

Query Match 100.0%; Score 27; DB 11; Length 122;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DYVIN 5  
|||||  
35 DYVIN 39

RESULT 11  
AAB64639 standard; Protein; 131 AA.  
ID AAB64639  
AC AAB64639;  
XX 22-MAR-2001 (first entry)  
XX Human secreted protein BLAST search protein SEQ ID NO: 149.  
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antileucic;  
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; human; secreted protein.  
XX Homo sapiens.  
XX WO200077197-A1.  
XX 21-DEC-2000.  
XX 01-JUN-2000; 2000WO-US14934.  
XX 11-JUN-1999; 99US-0138599.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX Rosen CA, Ruben SM, Komatsoulis GA;  
XX WPI; 2001-032312/04.  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
XX used in preventing, treating or ameliorating a medical condition -  
XX Disclosure; Page 534; 558pp; English.  
XX The invention relates to the isolation of genes AAF32757-F32803 encoding  
XX the human secreted proteins AAB64549-B64594. The sequence is a search  
XX result from a BLASTX homology search. The genes and proteins are useful  
XX for preventing, ameliorating or treating medical conditions, e.g. by  
XX protein or gene therapy. The genes are isolated from a range of human  
XX tissues disclosed in the specification. The nucleic acids, proteins,  
XX antibodies and (ant)agonists are useful in the diagnosis, treatment

CC and prevention of: (a) cancer, e.g. breast and ovarian cancer, and  
 CC other cancers of the adrenal gland, bone, bone marrow, breast,  
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound  
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
 CC and (f) infectious diseases such as viral, bacterial, fungal and  
 CC parasitic infections.  
 SQ Sequence 131 AA;

Query Match 100.0%; Score 27; DB 22; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 66 DYVIN 70

ULT 12  
 AAR04133  
 ID AAR04133 standard; protein; 136 AA.  
 AC AAR04133;

DT 06-SEP-1990 (first entry)

DE Anti-Leu 3a heavy chain variable region gene product, 316 vh.

KW HIV; AIDS; anti-Leu3A; vaccine; ds.

OS Mus musculus.

PN EP365209-A.

XX 25-APR-1990.

XX 11-OCT-1989; 89EP-ON10415.

XX 17-OCT-1988; 88US-0260558.

XX (BECT) BECTON DICKINSON CO.

PA Hinton R, Oi VT;

PI WPI; 1990-126329/17.

DR N-PSDB; AAQ04040.

PT New chimeric variants of murine antibody anti-leucine -  
 PT contg. human antibody regions, and DNA encoding sequences.  
 XX Claim 2; Fig 3; 12pp; English.

XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
 CC used to form chimeric mouse-variable, human-constant region Abs  
 CC suggested as being useful as a vaccine to HIV.  
 XX

SQ Sequence 136 AA;

Query Match 100.0%; Score 27; DB 11; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 49 DYVIN 53

RESULT 13  
 ABB68170

ID ABB68170 standard; Protein; 149 AA.  
 XX  
 AC ABB68170;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 31302.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 PI  
 XX WPI; 2001-656860/75.  
 DR N-PSDB; ABL12273.  
 DR  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 31302; 21pp + Sequence Listing; English.  
 CC  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB37737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 149 AA;  
 Query Match 100.0%; Score 27; DB 22; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 98;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 114 DYVIN 118

RESULT 14  
 ABB54572  
 ID ABB54572 standard; Protein; 303 AA.  
 XX  
 AC ABB54572;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Lactococcus lactis protein rlrA.  
 DE  
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
 KW Lactococcus lactis IL1403.  
 OS  
 XX Lactococcus lactis IL1403.  
 XX  
 PN FR2807446-A1.

Fri Feb 14 15:00:47 2003

CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain sequence of the antibody 4H5.  
 XX  
 SQ Sequence 305 AA;  
 Query Match 100.0%; Score 27; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DYVIN 5  
 Db 179 DYVIN 183  
 Search completed: February 14, 2003, 11:15:41  
 Job time : 14.5484 secs

XX 12-OCT-2001.  
 XX 11-APR-2000; 2000FR-0004630.  
 XX 11-APR-2000; 2000FR-0004630.  
 XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
 XX WPI; 2002-043418/06.  
 XX New nucleotide sequence useful in the identification of Lactococcus  
 PT lactis and related species -  
 XX Claim 6; SEQ ID No 1274; 2504pp; French.  
 The present invention is related to a Lactococcus lactis nucleotide  
 sequence (ABA90521) and related proteins (ABB53300-ABB55621). The  
 nucleic acid sequence is useful in the detection and/or amplification of  
 CC nucleic acid sequence, particularly to identify Lactococcus lactis or  
 CC related species. The proteins of the invention are useful for the  
 CC biosynthesis or biodegradation of a composition of interest. The  
 CC invention helps research in lactic bacteria, particularly useful in the  
 CC production of yogurt and cheese.  
 CC Note: The sequence data for this patent is based on equivalent patent  
 CC WO200177334 (published 18-OCT-2001) which is available in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 303 AA;  
 Query Match 100.0%; Score 27; DB 23; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DYVIN 5  
 Db 209 DYVIN 213  
 RESULT 15  
 AAY59264  
 ID AAY59264 standard; protein; 305 AA.  
 XX  
 AC AAY59264;  
 17-APR-2000 (first entry)  
 XX Antibody 4H5 H chain sequence.  
 XX CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX MUS SP.  
 XX JPI1332563-A.  
 XX 07-DEC-1999.  
 XX 26-MAY-1998; 98JP-0163034.  
 XX 26-MAY-1998; 98JP-0163034.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX WPI; 2000-091351/08.  
 XX N-PSDB; AAZ58663.  
 XX An antibody and the nucleic acid coding the antibody -  
 PT Disclosure; Page 16-17; 25pp; Japanese.  
 PS The invention provides an antibody having affinity to CD4 antigen. The  
 XX



Fri Feb 14 15:00:48 2003

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 ; Search time 4.51613 Seconds  
(without alignments)  
32.575 Million cell updates/sec

Title: US-09-701-001B-1  
Perfect score: 27  
Sequence: 1 DYVIN 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents-AA\*  
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2: /cgn2\_6/ptodata/1/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
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| 1          | 27    | 100.0       | 366    | 2     | US-08-804-699-2     |
| 2          | 27    | 100.0       | 990    | 4     | US-09-627-376-7     |
| 3          | 26    | 96.3        | 215    | 4     | US-09-247-373B-42   |
| 4          | 26    | 96.3        | 233    | 4     | US-09-134-001C-3845 |
| 5          | 26    | 96.3        | 238    | 2     | US-08-875-062-1     |
| 6          | 26    | 96.3        | 338    | 1     | US-08-606-888A-3    |
| 7          | 26    | 96.3        | 340    | 2     | US-08-355-844-1     |
| 8          | 26    | 96.3        | 340    | 5     | PCT-US95-16126-1    |
| 9          | 26    | 96.3        | 462    | 3     | US-09-238-796-2     |
| 10         | 26    | 96.3        | 525    | 4     | US-09-113-750A-35   |
| 11         | 26    | 96.3        | 575    | 1     | US-08-403-866-7     |
| 12         | 26    | 96.3        | 800    | 2     | US-08-785-052-4     |
| 13         | 26    | 96.3        | 800    | 2     | US-08-913-581-4     |
| 14         | 26    | 96.3        | 990    | 2     | US-08-352-625-20    |
| 15         | 26    | 96.3        | 990    | 2     | US-08-466-961A-20   |
| 16         | 26    | 96.3        | 990    | 2     | US-08-645-193B-15   |
| 17         | 26    | 96.3        | 2404   | 4     | US-09-134-001C-3464 |
| 18         | 25    | 92.6        | 7      | 6     | 5204096-28          |
| 19         | 25    | 92.6        | 127    | 4     | US-09-134-001C-3983 |
| 20         | 25    | 92.6        | 234    | 4     | US-09-384-162-9     |
| 21         | 25    | 92.6        | 327    | 4     | US-09-134-001C-4937 |
| 22         | 25    | 92.6        | 368    | 1     | US-08-423-399B-35   |
| 23         | 25    | 92.6        | 387    | 3     | US-08-935-263-6     |
| 24         | 25    | 92.6        | 387    | 4     | US-09-594-185-6     |
| 25         | 25    | 92.6        | 393    | 1     | US-08-423-399B-33   |
| 26         | 25    | 92.6        | 393    | 1     | US-08-530-950-11    |
| 27         | 25    | 92.6        | 393    | 4     | US-08-888-429A-11   |

|    |    |      |      |   |                     |                   |
|----|----|------|------|---|---------------------|-------------------|
| 28 | 25 | 92.6 | 393  | 4 | US-09-149-879-11    | Sequence 11, Appl |
| 29 | 25 | 92.6 | 400  | 1 | US-08-530-950-12    | Sequence 12, Appl |
| 30 | 25 | 92.6 | 400  | 2 | US-08-878-989-3     | Sequence 3, Appl  |
| 31 | 25 | 92.6 | 400  | 2 | US-08-878-989-17    | Sequence 17, Appl |
| 32 | 25 | 92.6 | 400  | 4 | US-08-888-429A-12   | Sequence 12, Appl |
| 33 | 25 | 92.6 | 400  | 4 | US-09-149-879-12    | Sequence 12, Appl |
| 34 | 25 | 92.6 | 400  | 4 | US-09-272-796-3     | Sequence 3, Appl  |
| 35 | 25 | 92.6 | 400  | 4 | US-09-272-796-17    | Sequence 17, Appl |
| 36 | 25 | 92.6 | 417  | 4 | US-09-134-001C-5006 | Sequence 5006, Ap |
| 37 | 25 | 92.6 | 522  | 4 | US-08-961-083-120   | Sequence 120, App |
| 38 | 25 | 92.6 | 736  | 4 | US-09-738-884-2     | Sequence 2, Appl  |
| 39 | 25 | 92.6 | 749  | 4 | US-09-562-737-98    | Sequence 98, Appl |
| 40 | 25 | 92.6 | 1040 | 4 | US-08-961-083-118   | Sequence 118, App |
| 41 | 25 | 92.6 | 1040 | 4 | US-08-576-626A-32   | Sequence 32, Appl |
| 42 | 24 | 88.9 | 223  | 4 | US-09-134-001C-3182 | Sequence 3182, Ap |
| 43 | 24 | 88.9 | 296  | 3 | US-08-986-769-2     | Sequence 2, Appl  |
| 44 | 24 | 88.9 | 362  | 4 | US-09-134-001C-5053 | Sequence 5053, Ap |
| 45 | 24 | 88.9 | 391  | 4 | US-09-134-001C-3952 | Sequence 3952, Ap |

ALIGNMENTS

RESULT 1  
US-08-804-699-2  
; Sequence 2, Application US/08804699  
; Patent No. 5854035  
; GENERAL INFORMATION:  
; APPLICANT: STOYAN, TANJA  
; TITLE OF INVENTION: ENZYME WITH LEUDH ACTIVITY, NUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCE CODING THEREFOR AND PROCESS FOR THE PREPARATION  
; TITLE OF INVENTION: OF THE ENZYME  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, L.L.P.  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,699  
; FILING DATE: 21-FEB-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JOYCE, KEVIN E  
; REGISTRATION NUMBER: 20,508  
; REFERENCE/DOCKET NUMBER: 21123/235920  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-804-699-2

Query Match 100.0%; Score 27; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYVIN 5  
|||||  
Db 285 DYVIN 289

## RESULT 2

US-09-627-376-7  
; Sequence 7, Application US/09627376  
; Patent No. 6342385  
; GENERAL INFORMATION:  
; APPLICANT: Qi, Fengxia      Caulfield, Page      Chen, Ping  
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS  
; FILE REFERENCE: UAB-17402/22  
; CURRENT APPLICATION NUMBER: US/09/627,376  
; CURRENT FILING DATE: 2001-05-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 990  
; TYPE: PRT  
; ORGANISM: Streptococcus mutans  
US-09-627-376-7

Query Match      100.0%;      Score 27;      DB 4;      Length 990;  
Best Local Similarity      100.0%;      Pred. No. 3.3e+02;  
Matches      5;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;  
QY      1 DYVIN 5  
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Db      185 DYVIN 189

## RESULT 3

US-09-247-373B-42  
; Sequence 42, Application US/09247373B  
; Patent No. 6168954  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1108-A  
; CURRENT APPLICATION NUMBER: US/09/247,373B  
; CURRENT FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 08/924,747  
; PRIOR FILING DATE: 1997-09-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 42  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: SOYBEAN  
US-09-247-373B-42

Query Match      96.3%;      Score 26;      DB 4;      Length 215;  
Best Local Similarity      80.0%;      Pred. No. 1e+02;  
Matches      4;      Conservative      1;      Mismatches      0;      Indels      0;      Gaps      0;

QY      1 DYVIN 5  
      |||||  
Db      173 DYVIN 177

## RESULT 4

US-09-134-001C-3845  
; Sequence 3845, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3845  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3845

Query Match      96.3%;      Score 26;      DB 4;      Length 233;  
Best Local Similarity      80.0%;      Pred. No. 1.1e+02;  
Matches      4;      Conservative      1;      Mismatches      0;      Indels      0;      Gaps      0;

QY      1 DYVIN 5  
      |||||  
Db      219 DYVIN 223

## RESULT 5

US-08-875-062-1  
; Sequence 1, Application US/08875062B  
; Patent No. 5942431  
; GENERAL INFORMATION:  
; APPLICANT: YONEDA, TADASHI  
; APPLICANT: HARUM, TAKADA  
; APPLICANT: KEI, OHNO  
; APPLICANT: JUNJI, SASUGA  
; TITLE OF INVENTION: NOVEL LIPASE GENE AND PROCESS FOR THE  
; TITLE OF INVENTION: PRODUCTION OF LIPASE WITH THE USE OF THE SAME  
; FILE REFERENCE: 5059.204  
; CURRENT APPLICATION NUMBER: US/08/875,062B  
; CURRENT FILING DATE: 1997-07-10  
; EARLIER APPLICATION NUMBER: PCT/JP96/00426  
; EARLIER FILING DATE: 1996-02-23  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Pseudomonas sp.  
US-08-875-062-1

Query Match      96.3%;      Score 26;      DB 2;      Length 288;  
Best Local Similarity      80.0%;      Pred. No. 1.4e+02;  
Matches      4;      Conservative      1;      Mismatches      0;      Indels      0;      Gaps      0;

QY      1 DYVIN 5  
      |||||  
Db      191 DYVIN 195

## RESULT 6

US-08-606-888A-3  
; Sequence 3, Application US/08606888A  
; Patent No. 5766913  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Shuen-Fuh  
; APPLICANT: Chiou, Chien-Ming  
; APPLICANT: Chuang, Kuang-Hsiang  
; TITLE OF INVENTION: CLONING, EXPRESSION AND NUCLEOTIDE  
; TITLE OF INVENTION: SEQUENCE OF A AKALINE GENE FROM PSEUDOMONAS  
; TITLE OF INVENTION: PSEUDOCALCIGENES F-III  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; ORGANISM: Escherichia coli
;
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..340
; OTHER INFORMATION: OmpF porin protein
;
US-08-355-844-1
    Query Match          96.3%; Score 26; DB 2; Length 340;
    Best Local Similarity 80.0%; Pred. No. 1.7e+02;
    Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYVIN 5
Db 312 DYVIN 316

RESULT 8
PCT-US95-16126-1
; Sequence 1, Application PC/TUS9516126
; GENERAL INFORMATION:
; APPLICANT: Fischbarg, Jorge
; APPLICANT: Czegledy, Ferenc
; APPLICANT: Iserovich, Pavel
; APPLICANT: Li, Jun
; APPLICANT: Cheung, Min
; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16126
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,844
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Tang, Henry Y.S.
; REGISTRATION NUMBER: 29,705
; REFERENCE/DOCKET NUMBER: A29927-50/29910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2586
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..340
; OTHER INFORMATION: OmpF porin protein
;
PCT-US95-16126-1
    Query Match          96.3%; Score 26; DB 5; Length 340;
    Best Local Similarity 80.0%; Pred. No. 1.7e+02;
    Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,888A
; FILING DATE: 26-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Rocky Y.
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 06840/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-8906
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
08-606-888A-3
    Query Match          96.3%; Score 26; DB 1; Length 338;
    Best Local Similarity 80.0%; Pred. No. 1.7e+02;
    Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYVIN 5
Db 241 DYVIN 245

RESULT 7
US-08-355-844-1
; Sequence 1, Application US/08355844
; Patent No. 5940307
; GENERAL INFORMATION:
; APPLICANT: Fischbarg, Jorge
; APPLICANT: Czegledy, Ferenc
; APPLICANT: Iserovich, Pavel
; APPLICANT: Li, Jun
; APPLICANT: Cheung, Min
; TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,844
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Tang, Henry Y.S.
; REGISTRATION NUMBER: 29,705
; REFERENCE/DOCKET NUMBER: A29927-50/29910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2586
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

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QY 1 DYVIN 5  
||:|  
Db 312 DYIIN 316

## RESULT 9

US-09-238-796-2  
; Sequence 2, Application US/09238796  
; Patent No. 6074845  
; GENERAL INFORMATION:  
; APPLICANT: AIYAR, NAMBI V.  
; TITLE OF INVENTION: BECLR:BOVINE CALCITONIN RECEPTOR-LIKE  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/238,796  
; FILING DATE: 28-JAN-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GP-70599  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0700  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 462 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; 09-238-796-2

Query Match 96.3%; Score 26; DB 3; Length 462;

Best Local Similarity 80.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
||:|  
Db 367 DYIIN 371

## RESULT 10

US-09-113-750A-35  
; Sequence 35, Application US/09113750A  
; Patent No. 6294176  
; GENERAL INFORMATION:  
; APPLICANT: David E. Junker and Mark D. Cochran  
; TITLE OF INVENTION: Recombinant Raccoonpox virus  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York

; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/113,750A  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 55744  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)262-0400  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 525 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-113-750A-35

Query Match 96.3%; Score 26; DB 4; Length 525;

Best Local Similarity 80.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
||:|  
Db 485 DYIIN 489

## RESULT 11

US-08-403-866-7  
; Sequence 7, Application US/08403866  
; Patent No. 5643779  
; GENERAL INFORMATION:  
; APPLICANT: Ehrlich, Stanislaw  
; APPLICANT: Godon, Jean-Jacques  
; APPLICANT: Renault, Pierre  
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate  
; TITLE OF INVENTION: synthase from Lactococcus and its applications  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,866  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 20747/30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1600  
; TELEFAX: (716) 263-1487  
; TELEX: 978450 (WUT)  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 575 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:



us-09-701-001b-1.ra1

Fri Feb 14 15:00:48 2003

ORGANISM: Lactococcus lactis subsp. lactis  
INDIVIDUAL ISOLATE: ILVB

US-08-403-866-7  
Query Match 96.3%; Score 26; DB 1; Length 575;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
Db 278 DYIN 282

RESULT 12  
US-08-785-052-4  
; Sequence 4, Application US/08785052  
; Patent No. 5756329

GENERAL INFORMATION:  
APPLICANT: Hodgson, John  
TITLE OF INVENTION: NO. 5756329el tRNA synthetase  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/785,052  
FILING DATE: 17-JAN-1997

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9601096.2  
FILING DATE: 19-JAN-1996  
APPLICATION NUMBER: 9615845.6  
FILING DATE: 27-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimml, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P31354-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090

TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 800 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-785-052-4

Query Match 96.3%; Score 26; DB 1; Length 800;  
Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
Db 607 DYVN 611

RESULT 13  
US-08-913-581-4  
; Sequence 4, Application US/08913581  
; Patent No. 5948657

GENERAL INFORMATION:  
APPLICANT: Hodgson, John  
TITLE OF INVENTION: NO. 5948657el tRNA Synthetase  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/913,581  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/785,052  
FILING DATE: 17-JAN-1997  
APPLICATION NUMBER: 9601096.2  
FILING DATE: 19-JAN-1996  
APPLICATION NUMBER: 9615845.6  
FILING DATE: 27-JUL-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Gimml, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P31354-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 800 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-913-581-4

Query Match 96.3%; Score 26; DB 2; Length 800;  
Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
Db 607 DYVN 611

RESULT 14  
US-08-392-625-20  
; Sequence 20, Application US/08392625  
; Patent No. 5837485

GENERAL INFORMATION:  
APPLICANT: Entian, Karl-Dieter  
APPLICANT: G tz, Friedrich  
APPLICANT: Schnell, No. 5837485bert  
APPLICANT: Augustin, Johannes  
APPLICANT: Engelke, Germar  
APPLICANT: Rosenstein, Ralf  
APPLICANT: Kaletta, Cortina  
APPLICANT: Klein, Cora  
APPLICANT: Wieland, Bernd  
APPLICANT: Kupke, Thomas  
APPLICANT: Jung, G nther  
APPLICANT: Kellner, Roland  
TITLE OF INVENTION: Biosynthetic Process For The Preparation  
; OF Chemical Compounds

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392.625  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/876,791  
FILING DATE: 30-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.0980002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 990 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-392-625-20

Query Match 96.3%; Score 26; DB 2; Length 990;  
Best Local Similarity 80.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
DB 248 DYIIN 252

RESULT 15  
US-08-466-961A-20  
Sequence 20, Application US/08466961A  
Patent No. 5843709  
GENERAL INFORMATION:  
APPLICANT: Entian, Karl-Dieter  
APPLICANT: G tz, Friedrich  
APPLICANT: Schnell, No. 5843709bert  
APPLICANT: Augustin, Johannes  
APPLICANT: Engelke, Germar  
APPLICANT: Rosenstein, Ralf  
APPLICANT: Kaletta, Cortina  
APPLICANT: Klein, Cora  
APPLICANT: Wieland, Bernd  
APPLICANT: Kupke, Thomas  
APPLICANT: Jung, G nther  
APPLICANT: Kellner, Roland  
TITLE OF INVENTION: Biosynthetic Process for the Preparation of  
TITLE OF INVENTION: Chemical Compounds  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,961A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392.625  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/876,791  
FILING DATE: 30-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/784,234  
FILING DATE: 31-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.0980004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 990 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-466-961A-20

Query Match 96.3%; Score 26; DB 2; Length 990;  
Best Local Similarity 80.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
DB 248 DYIIN 252

Search completed: February 14, 2003, 11:20:47  
Job time : 5.51613 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 : Search time 2.90323 Seconds  
(without alignments)  
44.001 Million cell updates/sec

Title: US-09-701-001b-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
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| 1          | 27    | 100.0       | 399    | 10    | US-09-925-301-1385  |
| 2          | 27    | 100.0       | 990    | 12    | US-10-047-676A-7    |
| 3          | 26    | 96.3        | 139    | 10    | US-09-815-242-10702 |
| 4          | 26    | 96.3        | 343    | 10    | US-09-815-242-5705  |
| 5          | 26    | 96.3        | 354    | 10    | US-09-815-242-12464 |
| 6          | 26    | 96.3        | 658    | 10    | US-09-815-242-10947 |
| 7          | 26    | 96.3        | 792    | 10    | US-09-815-242-5411  |
| 8          | 26    | 96.3        | 800    | 10    | US-09-815-242-12366 |
| 9          | 26    | 96.3        | 800    | 10    | US-09-815-242-12985 |
| 10         | 26    | 96.3        | 801    | 10    | US-09-815-242-4879  |
| 11         | 26    | 96.3        | 1167   | 10    | US-09-815-242-11522 |
| 12         | 26    | 96.3        | 1349   | 10    | US-09-815-242-5898  |
| 13         | 26    | 96.3        | 1349   | 10    | US-09-815-242-13137 |
| 14         | 25    | 92.6        | 118    | 10    | US-09-905-243-70    |
| 15         | 25    | 92.6        | 228    | 10    | US-09-755-665-38    |
| 16         | 25    | 92.6        | 276    | 10    | US-09-815-242-13118 |
| 17         | 25    | 92.6        | 306    | 10    | US-09-815-242-5895  |
| 18         | 25    | 92.6        | 364    | 10    | US-09-755-665-64    |
| 19         | 25    | 92.6        | 387    | 12    | US-10-033-078-6     |

Sequence 36, Appl  
Sequence 11, Appl  
Sequence 34, Appl  
Sequence 12, Appl  
Sequence 5329, Ap  
Sequence 12188, A  
Sequence 12845, A  
Sequence 381, App  
Sequence 120, App  
Sequence 69, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 118, App  
Sequence 5620, Ap  
Sequence 12543, A  
Sequence 31, Appl  
Sequence 5047, Ap  
Sequence 11770, A  
Sequence 10149, A  
Sequence 13845, A  
Sequence 88, Appl  
Sequence 13561, A  
Sequence 126, App  
Sequence 2, Appl  
Sequence 4, Appl  
Sequence 3, Appl

20 25 92.6 389 10 US-09-755-665-36  
21 25 92.6 393 10 US-09-761-569-11  
22 25 92.6 395 10 US-09-755-665-34  
23 25 92.6 400 10 US-09-761-569-12  
24 25 92.6 421 10 US-09-815-242-5329  
25 92.6 421 10 US-09-815-242-12188  
26 25 92.6 421 10 US-09-815-242-12845  
27 25 92.6 467 10 US-09-912-020-381  
28 25 92.6 522 10 US-09-765-272-120  
29 25 92.6 712 10 US-09-888-615-69  
30 25 92.6 736 9 US-10-096-961-2  
31 25 92.6 736 10 US-09-800-971-2  
32 25 92.6 1040 10 US-09-765-272-118  
33 24 88.9 157 10 US-09-815-242-5620  
34 24 88.9 157 10 US-09-815-242-12543  
35 24 88.9 170 10 US-09-775-925-31  
36 24 88.9 193 10 US-09-815-242-5047  
37 24 88.9 193 10 US-09-815-242-11770  
38 24 88.9 212 10 US-09-815-242-10149  
39 24 88.9 257 10 US-09-815-242-13845  
40 24 88.9 275 9 US-10-260-877-88  
41 24 88.9 296 10 US-09-815-242-13561  
42 24 88.9 361 9 US-09-989-442-126  
43 24 88.9 383 9 US-10-098-514-2  
44 24 88.9 383 9 US-10-098-514-4  
45 24 88.9 394 9 US-09-978-756-3

#### ALIGNMENTS

RESULT 1  
US-09-925-301-1385  
; Sequence 1385, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1385  
; LENGTH: 399  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1385

Query Match 100.0%; Score 27; DB 10; Length 399;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
Db 304 DYVIN 308  
|||||

RESULT 2  
US-10-047-676A-7  
; Sequence 7, Application US/10047676A  
; Patent No. US20020123105A1  
; GENERAL INFORMATION:  
; APPLICANT: Qi, Fengxia  
; APPLICANT: Caulfield, Page W.  
; APPLICANT: Chen, Ping W.  
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS  
; FILE REFERENCE: UAB-17403/22  
; CURRENT APPLICATION NUMBER: US/10/047,676A

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; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 990
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676A-7

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Query Match          100.0%; Score 27; DB 12; Length 990;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 DYVIN 5
Db 185 DYVIN 189

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RESULT 3
US-815-242-10702
Sequence 10702, Application US/09815242
Patent No. US20020061569A1

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; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A

```

```

; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10702
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10702

```

```

Query Match          96.3%; Score 26; DB 10; Length 139;
Best Local Similarity 80.0%; Pred. No. 40;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 DYVIN 5
Db 17 DYVIN 21

```

```

RESULT 4
US-09-815-242-5705
Sequence 5705, Application US/09815242
Patent No. US20020061569A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5705
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5705

```

```

Query Match          96.3%; Score 26; DB 10; Length 343;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 DYVIN 5
Db 210 DYVIN 214

```

```

RESULT 5
US-09-815-242-12464
Sequence 12464, Application US/09815242
Patent No. US20020061569A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

```

Fri Feb 14 15:00:48 2003

; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12464  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12464

Query Match 96.3%; Score 26; DB 10; Length 354;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||:|  
213 DYVIN 217

RESULT 6  
US-09-815-242-10947  
; Sequence 10947, Application US/09815242  
; Patent No. US20020061569A1

; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10947  
; LENGTH: 658  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-815-242-10947

Query Match 96.3%; Score 26; DB 10; Length 658;  
Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||:|  
76 DYVIN 80

RESULT 7  
US-09-815-242-5411  
; Sequence 5411, Application US/09815242

; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5411  
; LENGTH: 792  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-5411

Query Match 96.3%; Score 26; DB 10; Length 792;  
Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||:|  
Db 607 DYVIN 611

RESULT 8  
US-09-815-242-12366  
; Sequence 12366, Application US/09815242  
; Patent No. US20020061569A1

; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625

```

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12366
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12366

```

Query Match 96.3%; Score 26; DB 10; Length 800;  
Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels

ULT 9  
 US-09-815-242-12985  
 : Sequence 12985, Application US/09815242  
 : Patent No. US20020061569A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Haseibeck, Robert  
 : APPLICANT: Ohlsen, Kari L.  
 : APPLICANT: Zyskind, Judith W.  
 : APPLICANT: Wall, Daniel  
 : APPLICANT: Trawick, John D.  
 : APPLICANT: Carr, Grant J.  
 : APPLICANT: Yamamoto, Robert T.  
 : APPLICANT: Xu, H. Howard

```
Query Match          96.3%; Score 26; DB 10; Length 800;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
```

RESULT 10  
US-09-815-242-4879

```

; Sequence 4879, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

```
Query Match          96.3%; Score 26; DB 10; Length 801;
Best Local Similarity 80.0%; Pred. NO. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
```

RESULT 11  
US-09-815-242-11522  
; Sequence 11522, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

QY 1 DYN 5  
111.1  
Db 607 DYN 611

RESULT 10  
US-09-815-242-4879

us-09-701-001b-1.rapb

Fri Feb 14 15:00:48 2003

```

; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11522
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11522

```

```

Query Match          96.3%; Score 26; DB 10; Length 1167;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

1 DYVIN 5
11111
Db 1101 DYVIN 1105

```

```

RESULT 12
US-09-815-242-5898
; Sequence 5898, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5898
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5898

```

```

Query Match          96.3%; Score 26; DB 10; Length 1349;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

1 DYVIN 5
11111
Db 395 DYVIN 399

```

RESULT 13

```

US-09-815-242-13137
; Sequence 13137, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13137
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13137

```

```

Query Match          96.3%; Score 26; DB 10; Length 1349;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 DYVIN 5
11111
Db 395 DYVIN 399

```

```

RESULT 14
US-09-905-243-70
; Sequence 70, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat/chimpanzee sequence
US-09-905-243-70

```

```

Query Match          92.6%; Score 25; DB 10; Length 118;
Best Local Similarity 80.0%; Pred. No. 56;

```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||:|  
Db 31 DYVLN 35

## RESULT 15

US-09-755-665-38  
; Sequence 38, Application US/09755665  
; Patent No. US20020107186A1  
; GENERAL INFORMATION:  
; APPLICANT: Prayaga, Sudhirdas K.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tailon, Bruce E.  
; APPLICANT: Spaderna, Steven K.  
; APPLICANT: Spyttek, Kimberly A.  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-631  
; CURRENT APPLICATION NUMBER: US/09/755,665  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724  
; PRIOR FILING DATE: 2000-01-06  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-755-665-38

## Query Match

Best Local Similarity 92.6%; Score 25; DB 10; Length 228;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||:|  
Db 154 DYVIN 158

Search completed: February 14, 2003, 11:21:29  
Job time : 3.90323 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 5 Seconds  
(without alignments)

96.134 Million cell updates/sec

Title: US-09-701-001B-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 27    | 100.0       | 162    | 1 CFMWA  | C-phycocyanin alph |
| 2          | 27    | 100.0       | 162    | 2 T06968 | C-phycocyanin alph |
| 3          | 27    | 100.0       | 164    | 2 G45045 | phycoerythrin I al |
| 4          | 27    | 100.0       | 164    | 2 B35127 | phycoerythrin alph |
| 5          | 27    | 100.0       | 164    | 2 B47207 | phycoerythrin I al |
| 6          | 27    | 100.0       | 164    | 2 S43779 | phycoerythrin I al |
| 7          | 27    | 100.0       | 165    | 2 A40007 | phycoerythrin clas |
| 8          | 27    | 100.0       | 165    | 2 S25318 | phycoerythrin alph |
| 9          | 27    | 100.0       | 217    | 2 JS0492 | adenylate kinase ( |
| 10         | 27    | 100.0       | 217    | 2 T44404 | adenylate kinase ( |
| 11         | 27    | 100.0       | 231    | 2 D69980 | purine nucleoside  |
| 12         | 27    | 100.0       | 259    | 2 G81833 | hypothetical prote |
| 13         | 27    | 100.0       | 299    | 2 C90519 | hypothetical prote |
| 14         | 27    | 100.0       | 303    | 2 D86779 | LysR family transc |
| 15         | 27    | 100.0       | 341    | 2 D83217 | leucine dehydrogen |
| 16         | 27    | 100.0       | 345    | 2 E84051 | hypothetical prote |
| 17         | 27    | 100.0       | 347    | 1 A44245 | alcohol dehydrogen |
| 18         | 27    | 100.0       | 347    | 1 S51120 | alcohol dehydrogen |
| 19         | 27    | 100.0       | 348    | 2 H71110 | probable dehydroge |
| 20         | 27    | 100.0       | 348    | 2 G75049 | L-threonine 3-dehy |
| 21         | 27    | 100.0       | 353    | 2 A87507 | Glu/Leu/Phe/Val de |
| 22         | 27    | 100.0       | 353    | 2 A11859 | leucine dehydrogen |
| 23         | 27    | 100.0       | 364    | 1 B69962 | probable leucine d |
| 24         | 27    | 100.0       | 364    | 2 E83995 | leucine dehydrogen |
| 25         | 27    | 100.0       | 366    | 2 S45607 | leucine dehydrogen |
| 26         | 27    | 100.0       | 368    | 2 S54160 | spermine synthase  |
| 27         | 27    | 100.0       | 376    | 2 A89957 | hypothetical prote |
| 28         | 27    | 100.0       | 378    | 2 T25885 | hypothetical prote |
| 29         | 27    | 100.0       | 380    | 2 E81302 | probable type I re |

|    |    |       |     |          |                    |
|----|----|-------|-----|----------|--------------------|
| 30 | 27 | 100.0 | 386 | 2 D83284 | probable acyl-CoA  |
| 31 | 27 | 100.0 | 403 | 2 E70618 | probable fadE2 pro |
| 32 | 27 | 100.0 | 418 | 2 A97300 | gamma-glutamyl pho |
| 33 | 27 | 100.0 | 423 | 2 T15350 | hypothetical prote |
| 34 | 27 | 100.0 | 429 | 1 A31950 | leucine dehydrogen |
| 35 | 27 | 100.0 | 431 | 2 T36129 | probable PIS trans |
| 36 | 27 | 100.0 | 488 | 2 H71452 | hypothetical prote |
| 37 | 27 | 100.0 | 492 | 2 A97429 | flgK protein prote |
| 38 | 27 | 100.0 | 492 | 2 AB2647 | hook associated pr |
| 39 | 27 | 100.0 | 499 | 2 T32337 | hypothetical prote |
| 40 | 27 | 100.0 | 584 | 2 S27500 | xylanase - Prevote |
| 41 | 27 | 100.0 | 587 | 2 T27765 | hypothetical prote |
| 42 | 27 | 100.0 | 610 | 2 T35222 | hypothetical prote |
| 43 | 27 | 100.0 | 638 | 1 KQMSPL | plasma kallikrein  |
| 44 | 27 | 100.0 | 703 | 2 AC2430 | hypothetical prote |
| 45 | 27 | 100.0 | 705 | 2 S76729 | hypothetical prote |

## ALIGNMENTS

### RESULT 1

CFMWA

C-phycocyanin alpha chain - Fischerella sp.

C:Species: Fischerella sp.

C:Date: 30-Jun-1979 #sequence\_revision 30-Jun-1979 #text\_change 30-Apr-1999

C:Accession: A00315

R:Frank, G.; Sidler, W.; Widmer, H.; Zuber, H.

Hoppe-Sevler's Z. Physiol. Chem. 359, 1491-1507, 1978

A:Title: The complete amino acid sequence of both subunits of C-phycocyanin from the

A:Reference number: A00315; MUID:79087164; PMID:103794

A:Accession: A00315

A:Molecule type: protein

A:Residues: 1-162 <FRA>

A:Note: the source was designated as Mastigocladus laminosus

C:Superfamily: phycocyanin

C:Keywords: chromoprotein; photosynthesis; phycocyanobilin

F;84/Binding site: phycocyanobilin (Cys) (covalent) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 162;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYVIN 5

Db 155 DYVIN 159

### RESULT 2

T06968

C-phycocyanin alpha chain - Cyanophora paradoxa cyanelle

C:Species: cyanelle Cyanophora paradoxa

C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-Jun-1999

C:Accession: T06968; A24650

R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohmert, H.J.; Bryant, D.A.

submitted to the EMBL Data Library, July 1995

A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.

A:Reference number: Z15840

A:Accession: T06968

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-162 <STP>

A:Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81311.1; PID:g1016224

A:Experimental source: strain Pringsheim LB555

R:Lemaux, P.G.; Grossman, A.R.

EMBO J. 4, 1911-1919, 1985

A:Title: Major light-harvesting polypeptides encoded in polycistronic transcripts in

A:Reference number: A91009; MUID:86055745; PMID:2998775

A:Accession: A24650

A:Molecule type: DNA

A:Residues: 1-15 <LEM>

A:Cross-references: GB:X02790; NID:g11385; PIDN:CAA26557.1; PID:g11386

C:Genetics:

A:Gene: cpca  
 A:Genome: cyanelle  
 C:Superfamily: phycocyanin  
 C:Keywords: chromoprotein; cyanelle; heterodimer; photosynthesis; phycocyanobilin  
 F:84/Binding site: phycocyanobilin (Cys) (covalent) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 155 DYVIN 159

## RESULT 3

phycocerythrin I alpha chain - *Synechococcus* sp. (strain WH8020)  
 C:Species: *Synechococcus* sp.  
 C:Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Jun-1999  
 C:Accession: G45045; S31055

Wilbanks, S.M.; Glazer, A.N.  
 Biol. Chem. 268, 1236-1235, 1993  
 A:Title: Rod structure of a phycocerythrin II-containing phycobilisome. I. Organization a  
 chococcus sp. WH8020.

A:Reference number: A45045; MUID:93123238; PMID:8419325

A:Accession: G45045

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-164 <WIL>

A:Cross-references: EMBL:M95288; NID:g154551; PIDN:AAA27340.1; PID:g154560

A:Experimental source: WH8020

A>Note: sequence extracted from NCBI backbone (NCBIP:121981)

C:Genetics:

A:Gene: cpca

C:Superfamily: phycocyanin

Query Match 100.0%; Score 27; DB 2; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 157 DYVIN 161

## RESULT 4

phycocerythrin alpha chain - *Synechocystis* sp. (strain PCC 6701)  
 C:Species: *Synechocystis* sp.  
 C:Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 11-Jun-1999  
 C:Accession: B35127

R.Anderson, L.K.; Grossman, A.R.

J. Bacteriol. 172, 1297-1305, 1990

A:Title: Structure and light-regulated expression of phycocerythrin genes in wild-type an  
 A:Reference number: A35127; MUID:90170840; PMID:2106507

A:Accession: B35127

A:Molecule type: DNA

A:Residues: 1-164 <AND>

A:Cross-references: GB:M33812; NID:g154457; PIDN:AAA27280.1; PID:g154459

C:Superfamily: phycocyanin

Query Match 100.0%; Score 27; DB 2; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 157 DYVIN 161

## RESULT 5

B47207

phycocerythrin alpha subunit - red alga (*Rhodella violacea*)

C:Species: *Rhodella violacea*

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Feb-1997

C:Accession: B47207

R.Bernard, C.; Thomas, J.C.; Mazel, D.; Mousseau, A.; Castets, A.M.; Tandeau de Marsa

Proc. Natl. Acad. Sci. U.S.A. 89, 9564-9568, 1992

A:Title: Characterization of the genes encoding phycocerythrin in the red alga *Rhodell*

A:Reference number: A47207; MUID:93028502; PMID:1409666

A:Accession: B47207

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-164 <BER>

A>Note: sequence extracted from NCBI backbone (NCBIN:115792, NCBIP:115794)

C:Superfamily: phycocyanin

C:Keywords: chloroplast

Query Match 100.0%; Score 27; DB 2; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 157 DYVIN 161

## RESULT 6

S43779

phycocerythrin I alpha chain - *Synechococcus* sp.

C:Species: *Synechococcus* sp.

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 11-Jun-1999

C:Accession: S43779; S32642

R.Newman, J.; Mann, N.H.; Carr, N.G.

Plant Mol. Biol. 24, 679-683, 1994

A:Title: Organization and transcription of the class I phycocerythrin genes of the mar  
 A:Reference number: S43777; MUID:94207193; PMID:7512390

A:Accession: S43779

A:Molecule type: DNA

A:Residues: 1-164 <NEW>

A:Cross-references: EMBL:X72961; NID:g288983; PIDN:CAA51465.1; PID:g288986

C:Genetics:

A:Gene: cpca

C:Superfamily: phycocyanin

Query Match 100.0%; Score 27; DB 2; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 Db 157 DYVIN 161

## RESULT 7

A40007

phycocerythrin class II alpha chain mpeA - *Synechococcus* sp. (strain WH8020)

C:Species: *Synechococcus* sp.

C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 11-Jun-1999

C:Accession: A40007; S31048

R.Wilbanks, S.M.; de Lorimier, R.; Glazer, A.N.

J. Biol. Chem. 266, 9535-9539, 1991

A:Title: Phycocerythrins of marine unicellular cyanobacteria. Sequence of a class II p

A:Reference number: A40007; MUID:91236722; PMID:1903390

A:Accession: A40007

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <WIL>

A:Cross-references: GB:M61118; NID:g154529; PIDN:AAA27320.1; PID:g154531; EMBL:M95288

C:Genetics:

A:Gene: mpeA

C:Superfamily: phycocyanin

Query Match 100.0%; Score 27; DB 2; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

Db 158 DYVIN 162

# RESULT 8

S25318

phycoerythrin alpha chain - *Synechococcus* sp.

C:Species: *Synechococcus* sp.

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 28-May-1999

C:Accession: S25318

R:de Lorimier, R.; Chen, C.C.J.; Glazer, A.N.

Plant Mol. Biol. 20, 353-356, 1992

A:Title: Sequence comparison of two highly homologous phycoerythrins differing in bilin

A:Reference number: S25318; MUID:93004492; PMID:1391782

C:Accession: S25318

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <LOR>

A:Cross-references: GB:M91809; NID:gl54532; PIDN:AAA27322.1; PID:gl54534

C:Superfamily: phycocyanin

Query Match 100.0%; Score 27; DB 2; Length 165;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

Db 158 DYVIN 162

# RESULT 9

JS0492

adenylate kinase (EC 2.7.4.3) - *Bacillus subtilis*

N:Alternate names: ATP-AMP transphosphorylase

C:Species: *Bacillus subtilis*

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000

C:Accession: JS0492; S12684; S08630; E69583

R:Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yanane, K.

J. Biochem. 107, 603-607, 1990

A:Title: Cloning and characterization of a *Bacillus subtilis* gene homologous to *E. coli*

A:Reference number: JS0490; MUID:90292990; PMID:2113521

C:Accession: JS0492

A:Molecule type: DNA

A:Residues: 1-217 <NAK>

A:Cross-references: GB:D00619; NID:g216336; PIDN:BAA00496.1; PID:g216340

R:Yoshikawa, H.; Doi, R.H.

Nucleic Acids Res. 18, 1647, 1990

A:Title: Sequence of the *Bacillus subtilis* spectinomycin resistance gene region.

A:Reference number: S12680; MUID:90221911; PMID:2139212

C:Accession: S12684

A:Molecule type: DNA

A:Residues: 1-116 <YOS>

A:Cross-references: EMBL:M31102; NID:gl184272; PIDN:AAB59119.1; PID:gl43579

A:Experimental source: strain 1A241

R:Shih, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.

Mol. Microbiol. 4, 305-314, 1990

A:Title: Isolation of a *secY* homologue from *Bacillus subtilis*: evidence for a common pro

A:Reference number: S08628; MUID:90251170; PMID:2110998

C:Accession: S08630

A:Molecule type: DNA

A:Residues: 1-99 <SUH>

A:Cross-references: EMBL:X51329; NID:g40132; PIDN:CAA35713.1; PID:g40135

A:Experimental source: strain Marburg; cell line P2

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C:Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
riegler, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl  
A:Authors: Schlicht, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtili*  
A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69583

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-217 <KUN>

A:Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11913.1; PID:g26324

A:Experimental source: strain 168

C:Genetics:

A:Gene: adk

C:Function:

A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP

A:Note: magnesium required

C:Superfamily: adenylate kinase

C:Keywords: ATP; P-loop; phosphotransferase

F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical

F:80-85/Region: nucleotide-binding motif B #status atypical

F:28,84/Active site: His, Asp #status predicted

Query Match 100.0%; Score 27; DB 2; Length 217;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

Db 108 DYVIN 112

# RESULT 10

T44404

adenylate kinase (EC 2.7.4.3) [imported] - *Bacillus halodurans*

C:Species: *Bacillus halodurans*

C>Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 15-Jun-2001

C:Accession: T44404; C83669

R:Takami, H.; Takaki, Y.; Nakasone, K.; Hirama, C.; Inoue, A.; Horikoshi, K.

Biosci. Biotechnol. Biochem. 63, 452-455, 1999

A:Title: Sequence analysis of a 32-kb region including the major ribosomal protein ge

A:Reference number: Z2756; MUID:99209008; PMID:10192928

C:Accession: T44404

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-217 <TAK>

A:Cross-references: EMBL:AB017508; NID:g4512395; PIDN:BAA75292.1; PID:g4512425

A:Experimental source: strain C-125

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a

A:Reference number: A83650; MUID:20512582; PMID:11058132

C:Accession: C83669

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-217 <STO>

A:Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA03874.1; GSPDB:G

A:Experimental source: strain C-125

C:Genetics:

A:Gene: adk

C:Superfamily: adenylate kinase

C:Keywords: phosphotransferase

Query Match 100.0%; Score 27; DB 2; Length 217;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

Db 108 DYVIN 112

C90519  
Hypothetical protein MYP0\_0590 [imported] - Mycoplasma pulmonis (strain UAB CT1P)  
C:Species: Mycoplasma pulmonis  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 03-Aug-2001  
C:Accession: C90519  
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, P.  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p  
A:Reference number: A95512; MUID:21267165; PMID:11353084

A:Accession: C90519  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-299 <KUR>  
A:Cross-references: GB:AL445566; PID:g14089472; PIDN:CA013232.1; GSPDB:GN00153  
A:Experimental source: strain UAB Crip  
C:Genetics:  
A:Gene: MYPV\_0590  
A:Genetic code: SGC3

```

-
Db      73 DYVIN 77
      |||||
RESULT 14
D86779
LysR family transcription regulator [imported] - Lactococcus lactis subsp. lactis (st
C.Species: Lactococcus lactis subsp. lactis
C.Date: 23-Mar-2001 #sequence revision 23-Mar-2001 #text change 03-Aug-2001

```

Cv:Accession: D86779  
Cv:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich, S. P.; Artigues, C.; Delbecq, L.; et al.: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. cremoris strain B-12.  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. cremoris strain B-12.  
A:Reference number: A96625; MUID:21235186; PMID:11337471  
A:Accession: D86779  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-303 <STO>

A:Cross-References: GB:AE005176; PID:g12724207; PIDN:AAK05334.1; CSPDB:GN00146  
A:Experimental source: strain ILI403  
C:Genetics:  
A:Gene: rlrA  
Query Match 100.0%; Score 27; DB 2; Length 303;  
Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 209 DIVIN 213

RESULT 15

F83217

leucine dehydrogenase PA3418 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: F83217

A:Accession: F83217  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-341 <STO>

A;Residues: 1-341 <STO>  
A;Cross-references: GB:AE004763; GB:AE004091; NID:q9949556; PIDN:AG06806.1; GSPDB:GN

A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: ldh; PA3418  
 C:Superfamily: leucine dehydrogenase

Query Match 100.0%; Score 27; DB 2; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 |||||  
 Db 277 DYVIN 281

Search completed: February 14, 2003, 11:19:44  
 Job time : 6 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 2.58065 Seconds  
(without alignments)  
80.360 Million cell updates/sec

Title: US-09-701-001B-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 27    | 100.0       | 162    | 1 PHCA_CYPAA | P05730 cyanophora  |
| 2          | 27    | 100.0       | 162    | 1 PHCA_MASLA | P00307 mastigoclad |
| 3          | 27    | 100.0       | 164    | 1 PHAL_SYNPN | Q08086 synechococc |
| 4          | 27    | 100.0       | 164    | 1 PHAL_SYNPN | Q02179 synechococc |
| 5          | 27    | 100.0       | 164    | 1 PHEA_GRIMO | Q36005 griffithsia |
| 6          | 27    | 100.0       | 164    | 1 PHEA_RHOVL | Q02036 rhodella vi |
| 7          | 27    | 100.0       | 164    | 1 PHEA_SYN1  | P20778 synechocyst |
| 8          | 27    | 100.0       | 165    | 1 PHA2_SYNPN | P27646 synechococc |
| 9          | 27    | 100.0       | 165    | 1 PHA2_SYNPN | P37720 synechococc |
| 10         | 27    | 100.0       | 217    | 1 KAD_BACHD  | P38372 bacillus ha |
| 11         | 27    | 100.0       | 217    | 1 KAD_BACHD  | P16304 bacillus su |
| 12         | 27    | 100.0       | 231    | 1 MTN_BACSU  | Q32028 bacillus su |
| 13         | 27    | 100.0       | 280    | 1 ANFD_HEUGE | O88955 heliobacter |
| 14         | 27    | 100.0       | 347    | 1 ADH_SULSO  | P39462 sulfolobus  |
| 15         | 27    | 100.0       | 347    | 1 ADH_SULSR  | P50381 sulfolobus  |
| 16         | 27    | 100.0       | 364    | 1 DHLE_BACLI | Q53560 bacillus li |
| 17         | 27    | 100.0       | 364    | 1 DHLE_BACSU | P54531 bacillus su |
| 18         | 27    | 100.0       | 366    | 1 DHLE_BACCE | Q59194 bacillus ce |
| 19         | 27    | 100.0       | 366    | 1 DHLE_THEIN | O60030 thermoactin |
| 20         | 27    | 100.0       | 366    | 1 SPSY_HUMAN | P32788 homo sapien |
| 21         | 27    | 100.0       | 366    | 1 SPSY_MOUSE | P97355 mus musculu |
| 22         | 27    | 100.0       | 377    | 1 DHLE_BACST | P13154 bacillus st |
| 23         | 27    | 100.0       | 418    | 1 PROA_CLOAB | Q97e62 clostridium |
| 24         | 27    | 100.0       | 423    | 1 YW2_CAEEL  | Q11076 caenorhabdi |
| 25         | 27    | 100.0       | 587    | 1 YS48_CAEEL | Q09374 caenorhabdi |
| 26         | 27    | 100.0       | 638    | 1 KAL_MOUSE  | P26262 mus musculu |
| 27         | 27    | 100.0       | 820    | 1 SYL_CHLPN  | Q92930 chlamydia p |
| 28         | 27    | 100.0       | 857    | 1 GELA_DICDI | P13466 dictyosteli |
| 29         | 27    | 100.0       | 1082   | 1 RPOA_RORPC | P26190 porcine rot |
| 30         | 26    | 96.3        | 162    | 1 PHA3_FREDI | P14876 fremyella d |
| 31         | 26    | 96.3        | 164    | 1 PHEA_PORPU | P51368 porphyra pu |
| 32         | 26    | 96.3        | 168    | 1 RBS_CHLMO  | P17537 chlamydomon |
| 33         | 26    | 96.3        | 213    | 1 CAD1_DICDI | P54657 dictyosteli |

RESULT 1  
PHCA\_CYPAA STANDARD; PRT; 162 AA.  
AC P05730;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-phycocyanin alpha chain.  
GN CPCA OR PCYA.  
OS Cyanophora paradoxa.  
OG Cyanelle.  
OC Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.  
OX NCBI\_TaxID=2762;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LB555 / Pringsheim;  
RA Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,  
RA Bryant D.A.;  
RT "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";  
RL Plant Mol. Biol. Rep. 13:327-332(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LB555 / Pringsheim;  
RA Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,  
RA Farley J.F., Schlachter W.M., Chung S., Newmann-Spallart C.,  
RA Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;  
RT "The complete sequence of the cyanelle genome of Cyanophora paradoxa:  
RT the genetic complexity of a primitive plastid.";  
RL (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,  
RL Schwemmler W. (eds.);  
RL Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg  
RL (1997).  
RN [3]  
RP SEQUENCE OF 1-15 FROM N.A.  
RC MEDLINE=86055745; PubMed=2998775;  
RA Lemaux P.G., Grossman A.R.;  
RT "Major light-harvesting polypeptides encoded in polycistronic  
transcripts in a eukaryotic alga.";  
RL EMO J. 4:1911-1919(1985).  
CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN  
FROM THE PHYCOBILIPROTEIN COMPLEX.  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.  
CC -----  
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CC -----  
CC EMBL; U30821; AAA81311.1;  
CC PIR; A24650; CAA26557.1;  
CC HSP; P00306; 1PHN.

P17576 polyporus t  
O53872 streptomyce  
P02931 escherichia  
O69056 streptomyce  
Q06539 streptomyce  
P40176 streptomyce  
Q9uzw0 pyrococcus  
O58965 pyrococcus  
P42609 escherichia  
P14898 dictyoglomu  
Q02137 lactococcus  
P38882 saccharomyc

## ALIGNMENTS

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DR InterPro: IPR001659; Phycobilisome.
DR Pfam: PF00502; Phycobilisome; 1.
DR ProDom: PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
KW Cyanobacteria;
FT BINDING 84 84 PHYCOCYANOBILIN CHROMOPHORE
SQ SEQUENCE 162 AA; 17512 MW; 30BA91A389036AF4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 162;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5
Db 155 DYVIN 159

RESULT 2
PHCA_MASLA
ID PHCA_MASLA STANDARD; PRT; 162 AA.
P00307;
21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycocyanin alpha chain.
GN CPAC.
OS Mastigocladus laminosus (Fischerella sp.).
OC Bacteria; Cyanobacteria; Stigonematales; Fischerella.
OX NCBI_TaxID=1191;
RN [1]
RP SEQUENCE FROM N.A.
RA Kufer W., Hoegner A., Eberlein M., Mayer K., Buchner A.,
Gottschalk L.;
RT "Structure and molecular evolution of the gene cluster encoding
proteins of the rod substructure of the phycobilisome from the
cyanobacterium Mastigocladus laminosus".
RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE.
RX MEDLINE=79087164; PubMed=103794;
RA Frank G., Sidler W., Widmer H., Zuber H.;
RT "The complete amino acid sequence of both subunits of C-phycocyanin
from the cyanobacterium Mastigocladus laminosus".
RL Hoppe-Sevler's Z. Physiol. Chem. 359:1491-1507(1978).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCABILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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CC -----
DR EMBL: W75599; AAC64650.1; -.
DR PIR: A00315; CFMWA.
DR HSSP: P00306; LPHN.
DR InterPro: IPR001659; Phycobilisome.
DR Pfam: PF00502; Phycobilisome; 1.
DR ProDom: PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
FT INIT-MET 0 0
FT BINDING 84 84 PHYCOCYANOBILIN CHROMOPHORE.
FT CONFLICT 66 67 FT -> LI (IN REF. 2).
SQ SEQUENCE 162 AA; 17392 MW; B19F98565EA51E4AD CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 162;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5
Db 155 DYVIN 159

RESULT 3
PHAL_SYNPW
ID PHAL_SYNPW STANDARD; PRT; 164 AA.
Q08086;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycocerythrin class I alpha chain.
GN CPEA.
OS Synechococcus sp. (strain WH7803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32051;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94207193; PubMed=7512390;
RA Newman J., Mann N.H., Carr N.G.;
RT "Organization and transcription of the class I phycocerythrin genes of
the marine cyanobacterium Synechococcus sp. WH7803".
RL Plant Mol. Biol. 24:679-683(1994).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCABILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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CC -----
DR EMBL: X72961; CAA51465.1; -.
DR PIR: S32642; S32642.
DR PIR: S43779; S43779.
DR HSSP: O36005; LB8D.
DR InterPro: IPR001659; Phycobilisome.
DR Pfam: PF00502; Phycobilisome; 1.
DR ProDom: PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
FT BINDING 82 82 PHYCOCERYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCOCERYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17853 MW; B443CFD08C859D6A CRC64;

Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 164;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5
Db 157 DYVIN 161

RESULT 4
PHAL_SYNPY
ID PHAL_SYNPY STANDARD; PRT; 164 AA.
Q02179;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycocerythrin class I alpha chain.
GN CPEA.
OS Synechococcus sp. (strain WH8020).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32052;
RN [1]

```



SEQUENCE FROM N.A.  
 RX MEDLINE-93144698; PubMed-8425055;  
 RA de Lorinier R., Walbanks S.M., Glazer A.N.;  
 RT "Genes of the R-phycoerythrin II locus of marine *Synechococcus* spp.,  
 and comparison of protein-chromophore interactions in phycocyanins  
 RL differing in bilin composition.";  
 RL Plant Mol. Biol. 21:225-237(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93123238; PubMed-8419325;  
 RA Wilbanks S.M., Glazer A.N.;  
 RT "Rod structure of a phycoerythrin II-containing phycobilisome. I.  
 RT Organization and sequence of the gene cluster encoding the major  
 RT phycobiliprotein rod components in the genome of marine *Synechococcus*  
 RT sp. WH8020.";  
 RL J. Biol. Chem. 268:12226-12235(1993).  
 CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN  
 CC FROM THE PHYCOBILIPROTEIN COMPLEX.  
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.  
 CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.  
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 CC -----  
 DR EMBL; M95288; AAA27340.1; -;  
 DR PIR; G45045; G45045.  
 DR PIR; S31055; S31055.  
 DR HSP; O36005; 1B8D.  
 DR InterPro: IPR001659; Phycobilisome.  
 DR Pfam; PF00502; Phycobilisome; 1.  
 DR ProDom; PD000340; Phycobilisome; 1.  
 KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;  
 FT BINDING 82 82 PHYCOERYTHROBILIN CHROMOPHORE.  
 FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.  
 SQ SEQUENCE 164 AA; 17860 MW; 7AED0B19ED5F5D2C9 CRC64;  
 Query Match 100.0%; Score 27; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 DYVIN 5  
 157 DYVIN 161  
 RESULT 5  
 PHEA\_GRIMO STANDARD; PRT; 164 AA.  
 AC O36005;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE R-phycoerythrin alpha chain.  
 OS Griffithsia monilis.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiales;  
 OC Griffithsia.  
 OX NCBI\_TaxID=42003;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RA Rittner S., Hiller R.G., Sharples F.P., Wrench P.M., Welte W.,  
 RA Biederichs K.;  
 RT "Crystal structure of a phycoerythrin-containing phycoerythrin at  
 RT 1.90-A resolution.";  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases  
 CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN  
 CC FROM THE PHYCOBILIPROTEIN COMPLEX.

CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -!- SUBCELLULAR LOCATION: WITHIN THE THYLAKOID LUMEN. PERIPHERY OF THE  
 CC RODS OF THE PHYCOBILISOME.  
 CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.  
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 CC -----  
 DR EMBL; Z98528; CAB11029.1; -;  
 DR PDB; 1B8D; 18-FEB-99.  
 DR InterPro: IPR001659; Phycobilisome.  
 DR Pfam; PF00502; Phycobilisome; 1.  
 DR ProDom; PD000340; Phycobilisome; 1.  
 KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;  
 KW Chloroplast; 3D-structure.  
 FT BINDING 82 82 PHYCOERYTHROBILIN CHROMOPHORE.  
 FT BINDING 139 139 PHYCOERYTHROBILIN CHROMOPHORE.  
 SQ SEQUENCE 164 AA; 17669 MW; EFCF110AF760201A CRC64;  
 Query Match 100.0%; Score 27; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 DYVIN 5  
 157 DYVIN 161  
 RESULT 6  
 PHEA\_RHOVL STANDARD; PRT; 164 AA.  
 AC Q02036;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE B-phycoerythrin alpha chain.  
 GN CPEA OR RPEA.  
 OS Rhodella violacea.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;  
 OC Rhodella.  
 OX NCBI\_TaxID=2801;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93028502; PubMed-1409666;  
 RA Bernard C., Thomas J.C., Mazel D., Mousseau A., Castets A.M.,  
 RA Tandeau de Marsac N., Dubacq J.P.;  
 RT "Characterization of the genes encoding phycoerythrin in the red alga  
 RT Rhodella violacea: evidence for a splitting of the rpeB gene by an  
 RT intron.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9564-9568(1992).  
 CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN  
 CC FROM THE PHYCOBILIPROTEIN COMPLEX.  
 CC -!- SUBUNIT: HETEROPOLYMER OF 6 ALPHA, 6 BETA AND ONE GAMMA CHAINS.  
 CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.  
 CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.  
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 CC -----  
 DR EMBL; L02188; AAB01576.1; -;  
 DR PIR; B47207; B47207.  
 DR HSP; O36005; 1B8D.

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DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
KW Chloroplast. 82 82 PHYCORYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCORYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCORYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17696 MW; 6E8494D18B8204FC CRC64;

Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 157 DYVIN 161
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RESULT 7
PHEA_SYNP1
ID PHEA_SYNP1 STANDARD; PRT; 164 AA.
P20778:
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin alpha chain.
GN CPEA OR CPAA.
OS Synechocystis sp. (strain PCC 6701).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1144;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90170840; PubMed=2106507;
RA Anderson L.K., Grossman A.R.;
RT "Structure and light-regulated expression of phycoerythrin genes in
RT wild-type and phycobilisome assembly mutants of Synechocystis sp.
RT strain PCC 6701."
RL J. Bacteriol. 172:1297-1305(1990).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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EMBL; M33812; AAA27280.1; -
DR PIR; B35127; B35127.
DR HSP; O36005; IB8D.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
FT BINDING 82 82 PHYCORYTHROBILIN CHROMOPHORE.
FT BINDING 139 139 PHYCORYTHROBILIN CHROMOPHORE.
SQ SEQUENCE 164 AA; 17653 MW; 35CFB8503272E38F CRC64;

Query Match 100.0%; Score 27; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 157 DYVIN 161
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RESULT 8
PHEA_SYNP2

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PHA2_SYNPY
ID PHA2_SYNPY STANDARD; PRT; 165 AA.
P27646;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin class II alpha chain.
GN MPEA.
OS Synechococcus sp. (strain WH8020).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32052;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93144698; PubMed=8425055;
RA de Lorimier R., Wilbanks S.M., Glazer A.N.;
RT "Genes of the R-phycoerythrin II locus of marine Synechococcus spp.,
RT and comparison of protein-chromophore interactions in phycocyanins
RT differing in bilin composition."
RL Plant Mol. Biol. 21:225-237(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91236722; PubMed=1903390;
RA Wilbanks S.M., de Lorimier R., Glazer A.N.;
RT "Phycocerythrins of marine unicellular cyanobacteria. III. Sequence of
RT a class II phycoerythrin."
RL J. Biol. Chem. 266:9535-9539(1991).
RN [3]
RP CHROMOPHORES, AND PARTIAL SEQUENCE.
RX MEDLINE=91236720; PubMed=1903388;
RA Ong L.J., Glazer A.N.;
RT "Phycocerythrins of marine unicellular cyanobacteria. I. Bilin types
RT and locations and energy transfer pathways in Synechococcus spp.
RT phycoerythrins."
RL J. Biol. Chem. 266:9515-9527(1991).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobilisome.
CC -!- PTM: CONTAINS THREE COVALENTLY LINKED BILIN CHROMOPHORES.
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EMBL; M95288; AAA27333.1; -
DR PIR; A40007; A40007.
DR PIR; S31048; S31048.
DR HSP; O36005; IB8D.
DR InterPro; IPR001659; Phycobilisome.
DR Pfam; PF00502; Phycobilisome; 1.
DR ProDom; PD000340; Phycobilisome; 1.
KW Phycobilisome; Electron transport; Photosynthesis; Bile pigment.
FT BINDING 75 75 PHYCORYTHROBILIN CHROMOPHORE.
FT BINDING 83 83 PHYCORYTHROBILIN CHROMOPHORE 1.
FT BINDING 140 140 PHYCORYTHROBILIN CHROMOPHORE 2.
SQ SEQUENCE 165 AA; 17670 MW; B17A9C0BA5D24602 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 158 DYVIN 162
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RESULT 9
PHA2_SYNP2

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Fri Feb 14 15:00:49 2003

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RP PHA2_SYNPEZ STANDARD; PRT; 165 AA.
AC P37720;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-phycoerythrin class II alpha chain.
GN MPEA.
OS Synechococcus sp. (strain WH8103).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=29410;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93004492; PubMed=1391782;
RX de Lorimer R., Chen C.-J., Glazer A.N.;
RT "Sequence comparison of two highly homologous phycoerythrins
RL differing in bilin composition."
PL Plant Mol. Biol. 20:353-356(1992).
CC -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILIPROTEIN COMPLEX.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Periphery of the rods of the phycobillisome.
CC -!- PTM: CONTAINS THREE COVALENTLY LINKED BILIN CHROMOPHORES.
CC
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CC
CC EMBL: M91809; AAA27322.1; -
CC PIR: S25318; S25318.
CC HSSP: Q36005; LB8D.
CC InterPro: IPR001659; Phycobillisome.
CC Pfam: PF00502; Phycobillisome; 1.
CC ProDom: PD000340; Phycobillisome; 1.
CC Phycobillisome; Electron transport; Photosynthesis; Bile pigment.
KW BINDING 75 PHYCOUROBILIN CHROMOPHORE 1.
FT BINDING 83 PHYCOUROBILIN CHROMOPHORE 2.
FT BINDING 140 83 PHYCOUROBILIN CHROMOPHORE 3.
FT BINDING 140 140 PHYCOUROBILIN CHROMOPHORE 3.
SQ SEQUENCE 165 AA; 17729 MW; 17729 MW; DB 1; Length 165;
Query Match 100.0%; Score 27; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
11111
Db 158 DYVIN 162
RESULT 10
KAD_BACSD STANDARD; PRT; 217 AA.
ID KAD_BACSD Q9JWJ3; Q9JWJ3.
AC P38372; Q9JWJ3; Q9JWJ3.
DT 01-OCT-1994 (Rel. 30, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK OR BH0155.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=99209008; PubMed=10192928;
RT Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;
RT "Sequence analysis of a 32-kb region including the major ribosomal
RL protein gene clusters from alkaliphilic Bacillus sp. strain C-125.";
RL Biosci. Biotechnol. Biochem. 63:452-455(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RT Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
RN [3]
RP SEQUENCE OF 1-107 FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=92381482; PubMed=1512566;
RA Kang S.K., Kudo T., Horikoshi K.;
RT "Molecular cloning and characterization of an alkalophilic Bacillus
RT sp. C125 gene homologous to Bacillus subtilis secY.";
RL J. Gen. Microbiol. 138:1363-1370(1992).
CC -!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB017508; BAA75292.1; -
CC PIR: AP01507; BAB03874.1; -
CC HSSP: D10360; BAA01192.1; -
CC InterPro: IPR000850; Adenylate_kin.
CC Pfam: PF00406; adenylatekinase; 1.
CC ProDom: PD00094; ADENYLATE_KINASE.
CC ProDom: PD000657; Adenylate_kin; 1.
CC PROSITE: PS00113; ADENYLATE_KINASE; 1.
CC Transferase; Kinase; ATP-binding; Complete proteome.
KW NP-BIND 7 4 I -> N (IN REF. 3).
FT CONFLICT 15 ATP (BY SIMILARITY).
SQ SEQUENCE 217 AA; 24170 MW; FD5DF854B3BA3592 CRC64;
Query Match 100.0%; Score 27; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DYVIN 5
11111
Db 108 DYVIN 112
RESULT 11
KAD_BACSD STANDARD; PRT; 217 AA.
ID KAD_BACSD Q9JWJ3; Q9JWJ3.
AC P16304;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN ADK.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90292990; PubMed=2113521;
RT Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.;
RN Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.;
```

RT "Cloning and characterization of a Bacillus subtilis gene homologous  
 RL to E. coli secY.";  
 RJ J. Biochem. 107:603-607(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / Marburg;  
 RX MEDLINE=96186897; PubMed=8635744;  
 RA Suh J.W., Boylan S.A., Oh S.H., Price C.W.;  
 RT "Genetic and transcriptional organization of the Bacillus subtilis  
 RL spc-alpha region.";  
 RN Gene 169:17-23(1996).  
 RP [3]  
 RC SEQUENCE OF 1-116 FROM N.A.  
 RX MEDLINE=90221911; PubMed=2139212;  
 RA Yoshikawa H., Doi R.H.;  
 RT "Sequence of the Bacillus subtilis spectinomycin resistance gene  
 RL region.";  
 RN Nucleic Acids Res. 18:1647-1647(1990).  
 RP [4]  
 RC SEQUENCE OF 1-99 FROM N.A.  
 RX STRAIN=168;  
 RA Suh J.W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,  
 RT Price C.W.;  
 RL "Isolation of a secY homologue from Bacillus subtilis: evidence for a  
 common protein export pathway in eubacteria.";  
 RN Mol. Microbiol. 4:305-314(1990).  
 RP SEQUENCE OF 1-20.  
 RC STRAIN=168 / IS58;  
 RX MEDLINE=97443988; PubMed=9298659;  
 RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,  
 RT Hecker M.;  
 RL "First steps from a two-dimensional protein index towards a response-  
 RT regulation map for Bacillus subtilis.";  
 RN Electrophoresis 18:1451-1463(1997).  
 CC -!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR  
 CC MAINTENANCE AND CELL GROWTH.  
 CC -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: BY SUPEROXIDE.  
 CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; D00619; BAA00496.1; -;  
 DR EMBL; L47971; AAB06820.1; -;  
 DR EMBL; M31102; AAB59119.1; -;  
 DR EMBL; X51329; CAA35713.1; -;  
 DR EMBL; Z99104; CAB11913.1; -;  
 DR PIR; JS0492; JS0492; -;  
 DR PIR; S08630; S08630; -;  
 DR PIR; S12684; S12684; -;  
 DR HSSP; P27142; IZIN.  
 DR Subtilist; BG10446; adk.  
 DR InterPro; IPR000850; Adenylate\_kin.  
 DR Pfam; PF00406; adenylatekinase; 1.  
 DR PRINTS; PR00094; ADENYLTKINASE.  
 DR ProDom; PD000657; Adenylate\_kin; 1.  
 DR PROSITE; P500113; ADENYLATE\_KINASE; 1.  
 KW Transferase; Kinase; ATP-binding; Complete proteome.  
 FT NP\_BIND 7 15 ATP (BY SIMILARITY).  
 SQ SEQUENCE 217 AA; 24119 MW; ECD9ECF4F26A1E90 CRC64;

\* Query Match

Best Local Similarity 100.08; Score 27; DB 1; Length 217;  
 Pred. No. 33;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DYVIN 5  
 Db 108 DYVIN 112  
 RESULT 12  
 MTN\_BACSU STANDARD; PRT; 231 AA.  
 ID MTN\_BACSU  
 AC O32028;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE MTA/SAH nucleosidase [Includes: 5'-methylthioadenosine nucleosidase  
 DE (EC 3.2.2.15); S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)].  
 GN MTN OR PFS.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
 RA Gusepht G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaer-Bianchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Medina N., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenger T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,  
 RT subtilis";  
 RL "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RL Nature 390:249-256(1997).  
 CC -!- FUNCTION: RESPONSIBLE FOR CLEAVAGE OF THE GLYCOSIDIC BOND IN BOTH  
 CC 5'-METHYLTHIOADENOSINE (MTA) AND S-ADENOSYLHOMOCYSTEINE (SAH) (BY  
 CC SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = adenine +  
 CC S-D-ribosyl-L-homocysteine.  
 CC -!- CATALYTIC ACTIVITY: Methylthioadenosine + H(2)O = adenine + 5-  
 CC methylthio-D-ribose.  
 CC -!- SIMILARITY: BELONGS TO THE MTN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; Z99117; CAB14669.1; -;

DR SubtilList; BGI3800; mtm.  
DR InterPro; IPR000845; PNP\_UDP.  
DR Pfam; PF01048; PNP\_UDP\_1; 1.  
DR ProDom; PD003928; PNP\_UDP; 1.  
KW Hydrolase; Multifunctional enzyme; Complete proteome.  
SQ SEQUENCE 231 AA; 25264 MW; 7F6B8BC8EDA1E728 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 231;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5  
|||||  
Db 69 DYVIN 73

RESULT 13  
ADH\_SULSO STANDARD; PRT; 280 AA.  
O68955;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Nitrogenase iron-iron protein alpha chain (EC 1.18.6.1) (Nitrogenase  
DE component I) (Dinitrogenase 3 alpha subunit) (Fragment).  
GN ANFD.  
OS Hellobacterium gestii.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Hellobacteriaceae;  
OC Hellobacterium.  
OX NCBI\_TaxID=2699;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Loveless T.M., Bishop P.E.;  
RT Identification of genes unique to Mo-independent nitrogenase systems  
RT in diverse diazotrophs.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THE KEY ENZYMAIC REACTIONS IN NITROGEN FIXATION ARE  
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE  
CC IRON PROTEIN (COMPONENT 2) AND A COMPONENT 1 WHICH IS EITHER A  
CC MOLYBDENUM-IRON PROTEIN, A VANADIUM-IRON, OR AN IRON-IRON PROTEIN.  
CC -!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP  
CC = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.  
CC -!- COFACTOR: IRON-SULFUR (BY SIMILARITY).  
CC -!- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO DELTA CHAINS (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.  
CC  
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CC  
CC EMBL; AF058785; AAC14342.1; -;  
CC HSSP; P00467; 1MIO.  
CC InterPro; IPR000318; Nitrogense\_comp1.  
CC InterPro; IPR000510; Oxred\_nitrogensel.  
CC Pfam; PF00148; oxidored\_nitro; 1.  
CC TIGRFAMs; TIGR01284; alt\_nitrog\_alph; 1.  
CC PROSITE; PS00090; NITROGENASE\_1\_2; 1.  
CC PROSITE; PS00699; NITROGENASE\_1\_1; 1.  
KW Oxidoreductase; Nitrogen fixation; Iron-sulfur.  
FT NON\_TER 1 280  
FT NON\_TER 280 280  
SQ SEQUENCE 280 AA; 31772 MW; CDF253376AF1056A1 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 280;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

Db 158 DYVIN 162  
|||||

RESULT 14  
ADH\_SULSO STANDARD; PRT; 347 AA.  
AC P39462; O74076;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE NAD-dependent alcohol dehydrogenase (EC 1.1.1.1).  
GN ADH OR SSO2536.  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN-ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=93099126; PubMed=1463738;  
RA Amendola S., Raia C.A., Caruso C., Camardella L., D'Auria S.,  
RA de Rosa M., Rossi M.;  
RT "Thermostable NAD(+)-dependent alcohol dehydrogenase from Sulfolobus  
RT solfataricus: gene and protein sequence determination and  
RT relationship to other alcohol dehydrogenases.";  
RL Biochemistry 31:12514-12523(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 35092 / DSM 1617 / P2;  
RA Aravalli R.N.;  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She Q., Singh R.K., Confalonieri F., Zivanovic V., Allard G.,  
RA Awey M.A., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moors A., Eranosky G., Fletcher C., Gordon P.M.K.,  
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
RA Garrett R.A., Ragan M.A., Sensesen C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +  
CC NADH.  
CC -!- COFACTOR: ZINC; BINDS 4 ZINC IONS PER DIMER.  
CC -!- SUBUNIT: HOMODIMER AND HOMOTETRAMER.  
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE  
CC FAMILY.  
CC  
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CC  
CC EMBL; S51211; AAB24546.1; -;  
CC EMBL; AJ010590; CAA09258.1; -;  
CC EMBL; AE006850; AAR42665.1; -;  
CC PIR; A44245; A44245.  
CC InterPro; IPR002328; ADH\_zinc.  
CC InterPro; IPR002085; adh\_zn\_family.  
CC InterPro; IPR000051; SAM\_bind.  
CC Pfam; PF00107; adh\_zinc; 1.  
CC PROSITE; PS00059; ADH\_ZINC; 1.  
KW Oxidoreductase; Zinc; NAD; Methylation; Complete proteome.  
FT MOD\_RES 11 11  
FT MOD\_RES 213 213 METHYLATION.  
FT METAL 38 38 ZINC (CATALYTIC) (BY SIMILARITY).  
FT

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FT METAL 68 68 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 98 98 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 101 101 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 104 104 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 112 112 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 154 154 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 347 AA; 37568 MW; 755848A249D4F4A2 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
Db 218 DYVIN 222

RESULT 15
ADH_SULSR STANDARD; PRT; 347 AA.
AC P50381;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE NAD-dependent alcohol dehydrogenase (EC 1.1.1.1).
GN ADH.
OS Sulfolobus sp. (strain RC3).
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=165757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96125263; PubMed=8550434;
RA Cannio R., Fiorentino G., Carpinelli P., Rossi M., Bartolucci S.;
RT "Cloning and overexpression in Escherichia coli of the genes encoding
RL NAD-dependent alcohol dehydrogenase from two Sulfolobus species.";
RL J. Bacteriol. 178:301-305(1996).
CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
CC NADH.
CC -!- COFACTOR: ZINC; BINDS 4 ZINC IONS PER DIMER.
CC -!- SUBUNIT: HOMODIMER AND HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; Z47543; CAAB7591.1; -.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF00107; adh_zinc; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; NAD; Methylation.
FT MOD_RES 11 11 METHYLATION (BY SIMILARITY).
FT MOD_RES 213 213 METHYLATION (BY SIMILARITY).
FT METAL 38 38 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 68 68 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 98 98 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 101 101 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 104 104 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 112 112 ZINC (SECOND ATOM) (BY SIMILARITY).
FT METAL 154 154 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 347 AA; 37583 MW; 55D3C003792DE60D CRC64;

Query Match 100.0%; Score 27; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYVIN 5  
Db 218 DYVIN 222

Search completed: February 14, 2003, 11:16:19  
Job time : 3.58065 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 10.4032 Seconds  
(without alignments)  
99.030 Million cell updates/sec

Title: US-09-701-001B-1

Perfect score: 27

Sequence: 1 DYVIN 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues ; 671580  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL\_21.\*
- 2: sp\_archaea.\*
- 3: sp\_bacteria.\*
- 4: sp\_fungi.\*
- 5: sp\_human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mammal.\*
- 8: sp\_mhc.\*
- 9: sp\_organelle.\*
- 10: sp\_phage.\*
- 11: sp\_plant.\*
- 12: sp\_rodent.\*
- 13: sp\_virus.\*
- 14: sp\_vertebrate.\*
- 15: sp\_unclassified.\*
- 16: sp\_virus.\*
- 17: sp\_bacteriap.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query % | Length | ID        | Description        |
|------------|-------|---------|--------|-----------|--------------------|
| 1          | 27    | 100.0   | 82     | 2 Q9L4G6  | Q9L4G6 streptococ  |
| 2          | 27    | 100.0   | 113    | 5 Q9VEV5  | Q9VEV5 drosophila  |
| 3          | 27    | 100.0   | 149    | 5 Q9V965  | Q9V965 drosophila  |
| 4          | 27    | 100.0   | 185    | 12 Q9EMY1 | Q9EMY1 amsacta moo |
| 5          | 27    | 100.0   | 197    | 17 Q8U241 | Q8U241 pyrococcus  |
| 6          | 27    | 100.0   | 231    | 8 Q9MJ64  | Q9MJ64 physarum po |
| 7          | 27    | 100.0   | 258    | 11 Q9R282 | Q9R282 mus musculu |
| 8          | 27    | 100.0   | 259    | 16 Q9RQW0 | Q9RQW0 neisseria m |
| 9          | 27    | 100.0   | 298    | 16 Q98I60 | Q98I60 rhizobium l |
| 10         | 27    | 100.0   | 299    | 16 Q98RF0 | Q98RF0 mycoplasma  |
| 11         | 27    | 100.0   | 303    | 16 Q9CG74 | Q9CG74 lactococcus |
| 12         | 27    | 100.0   | 341    | 16 Q9HV17 | Q9HV17 pseudomonas |
| 13         | 27    | 100.0   | 345    | 16 Q9K724 | Q9K724 bacillus ha |
| 14         | 27    | 100.0   | 347    | 17 Q96XE0 | Q96XE0 sulfolobus  |
| 15         | 27    | 100.0   | 348    | 17 Q58389 | Q58389 pyrococcus  |
| 16         | 27    | 100.0   | 348    | 17 Q9UYX0 | Q9UYX0 pyrococcus  |

|    |    |       |     |           |                      |
|----|----|-------|-----|-----------|----------------------|
| 17 | 27 | 100.0 | 348 | 17 Q8U259 | Q8U259 pyrococcus    |
| 18 | 27 | 100.0 | 349 | 4 Q9UQS1  | Q9UQS1 homo sapien   |
| 19 | 27 | 100.0 | 353 | 16 Q9A6L1 | Q9A6L1 caulobacter   |
| 20 | 27 | 100.0 | 353 | 16 Q8YZN1 | Q8YZN1 anabaena sp   |
| 21 | 27 | 100.0 | 357 | 2 Q85768  | Q85768 legionella    |
| 22 | 27 | 100.0 | 359 | 13 Q9YH97 | Q9YH97 tetraodon f   |
| 23 | 27 | 100.0 | 359 | 13 Q9YH96 | Q9YH96 fugu rubrip   |
| 24 | 27 | 100.0 | 360 | 13 Q9YGC9 | Q9YGC9 brachydanio   |
| 25 | 27 | 100.0 | 364 | 16 Q9K985 | Q9K985 bacillus ha   |
| 26 | 27 | 100.0 | 376 | 16 Q99TD9 | Q99TD9 staphylococ   |
| 27 | 27 | 100.0 | 380 | 2 Q8RN27  | Q8RN27 campylobact   |
| 28 | 27 | 100.0 | 380 | 16 Q9PMB8 | Q9PMB8 campylobact   |
| 29 | 27 | 100.0 | 386 | 16 Q9HZV8 | Q9HZV8 pseudomonas   |
| 30 | 27 | 100.0 | 399 | 5 Q9NC97  | Q9NC97 trypanosoma   |
| 31 | 27 | 100.0 | 407 | 16 Q96831 | Q96831 mycobacteri   |
| 32 | 27 | 100.0 | 420 | 16 Q8XXU3 | Q8XXU3 raltestonia s |
| 33 | 27 | 100.0 | 423 | 16 Q9CNX7 | Q9CNX7 paleurella    |
| 34 | 27 | 100.0 | 431 | 16 Q9S2H5 | Q9S2H5 streptomyce   |
| 35 | 27 | 100.0 | 444 | 16 Q9A1M4 | Q9A1M4 streptococ    |
| 36 | 27 | 100.0 | 464 | 5 Q01607  | Q01607 caenorhabdi   |
| 37 | 27 | 100.0 | 488 | 17 Q58017 | Q58017 pyrococcus    |
| 38 | 27 | 100.0 | 488 | 17 Q8WZP5 | Q8WZP5 pyrococcus    |
| 39 | 27 | 100.0 | 492 | 16 Q8UHV4 | Q8UHV4 agrobacteri   |
| 40 | 27 | 100.0 | 520 | 5 Q17175  | Q17175 caenorhabdi   |
| 41 | 27 | 100.0 | 543 | 5 Q9V7R9  | Q9V7R9 drosophila    |
| 42 | 27 | 100.0 | 584 | 2 Q45397  | Q45397 prevotella    |
| 43 | 27 | 100.0 | 593 | 17 Q97BL5 | Q97BL5 thermoplasm   |
| 44 | 27 | 100.0 | 610 | 16 Q86712 | Q86712 streptomyce   |
| 45 | 27 | 100.0 | 616 | 5 Q9V7P8  | Q9V7P8 drosophila    |

## ALIGNMENTS

RESULT 1

| ID | Q9L4G6   | PRELIMINARY; | PRT; | 82 AA. |
|----|--|--------------|------|--------|
| AC | Q9L4G6;  |              |      |        |
| DT | 01-OCT-2000 (TReMBLrel. 15, Created)                                   |              |      |        |
| DT | 01-OCT-2000 (TReMBLrel. 15, Last sequence update)                      |              |      |        |
| DT | 01-DEC-2001 (TReMBLrel. 19, Last annotation update)                    |              |      |        |
| DE | Xis (Excisionase).   |              |      |        |
| GN | XIS.   |              |      |        |
| OS | Streptococcus thermophilus.  |              |      |        |
| OC | Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;     |              |      |        |
| OC | Streptococcaceae; Streptococcus.                                       |              |      |        |
| OX | NCBI_TaxID=1308;   |              |      |        |
| RN | [1]  |              |      |        |
| RP | SEQUENCE FROM N.A.   |              |      |        |
| RC | STRAIN=CNRZ368;  |              |      |        |
| RC | MEDLINE=20208895; PubMed=10742276;                                     |              |      |        |
| RA | Burris V., Roussel Y., Decaris B., Guedon G.;                          |              |      |        |
| RA | "Characterization of a novel integrative element, ICEstl, in the       |              |      |        |
| RT | lactic acid bacterium streptococcus thermophilus.;"                    |              |      |        |
| RL | Appl. Environ. Microbiol. 66:1749-1753(2000).                          |              |      |        |
| RN | [2]  |              |      |        |
| RP | SEQUENCE FROM N.A.   |              |      |        |
| RC | STRAIN=CNRZ368;  |              |      |        |
| RC | MEDLINE=95379495; PubMed=7651138;                                      |              |      |        |
| RA | Guedon G., Bourgoin F., Pebay M., Roussel Y., Colmin C., Simonet J.M., |              |      |        |
| RA | Decaris B.;  |              |      |        |
| RT | "Characterization and distribution of two insertion sequences, IS1191  |              |      |        |
| RT | and iso-IS981, in Streptococcus thermophilus: does intergeneric        |              |      |        |
| RT | transfer of insertion sequences occur in lactic acid bacteria co-      |              |      |        |
| RT | cultures?";  |              |      |        |
| RL | Mol. Microbiol. 16:69-78(1995).  |              |      |        |
| RN | [3]  |              |      |        |
| RP | SEQUENCE FROM N.A.   |              |      |        |
| RC | STRAIN=CNRZ368;  |              |      |        |
| RC | MEDLINE=97286550; PubMed=9141697;                                      |              |      |        |
| RA | Roussel Y., Bourgoin F., Guedon G., Pebay M., Decaris B.;              |              |      |        |
| RT | "Analysis of the genetic polymorphism between three Streptococcus      |              |      |        |
| RT | thermophilus strains by comparing their physical and genetic           |              |      |        |

RT organization.";  
 RL Microbiology 143:1335-1343(1997).  
 DR EMBL; AJ243106; CAB70621.1; -  
 DR EMBL; AJ278471; CAC67553.1; -  
 SQ SEQUENCE 82 AA; 9901 MW; 1681678702142DFD CRC64;

Query Match 100.0%; Score 27; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 |||||  
 Db 49 DYVIN 53

## RESULT 2

Q9V965 PRELIMINARY; PRT; 113 AA.  
 AC Q9V965  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 CG10406 protein.  
 MRPS33 OR CG10406.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003713; AAF55312.1; -  
 DR FlyBase; FBgn0038426; mrps33.

SQ SEQUENCE 113 AA; 13685 MW; 1943154BABDB2926 CRC64;

Query Match 100.0%; Score 27; DB 5; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
 |||||  
 Db 54 DYVIN 58

## RESULT 3

Q9V965 PRELIMINARY; PRT; 149 AA.  
 AC Q9V965  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE CG13437 protein.  
 GN CG13437  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003791; AAF57432.1; -  
 DR FlyBase; FBgn0034541; CG13437.  
 SQ SEQUENCE 149 AA; 17627 MW; 095FFAA04D7EA12F CRC64;

Query Match 100.0%; Score 27; DB 5; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;



Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||||  
Db 114 DYVIN 118

## RESULT 4

Q9EMY1 PRELIMINARY; PRT; 185 AA.  
AC Q9EMY1  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE AMV068.  
GN AMV068.  
OS Anaseta moorei entomopoxvirus (AmEPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
OC Entomopoxvirus B.  
OX NCBI\_TaxID=28321;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20396580; PubMed=10936094;  
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RT "Complete Genomic Sequence of the Anaseta moorei Entomopoxvirus;  
RT Analysis and Comparison with Other Poxviruses.";  
RL Virology 274:120-139(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,  
Moyer R.W.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR ENBL: AF250284; AAG02774.1; -  
SQ SEQUENCE 185 AA; 21994 MW; FD9F960A83DFF033 CRC64;

Query Match 100.0%; Score 27; DB 12; Length 185;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||||  
Db 71 DYVIN 75

## RESULT 5

Q8U241 PRELIMINARY; PRT; 197 AA.  
AC Q8U241  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Hypothetical protein PF1009.  
GN PF1009.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;  
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
RT "The complete sequence of the Pyrococcus furiosus genome.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR ENBL: AE010212; AAL81133.1; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 197 AA; 23432 MW; 516CB4985B1E083B CRC64;

Query Match 100.0%; Score 27; DB 17; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||  
Db 18 DYVIN 22

## RESULT 6

Q9MJ64 PRELIMINARY; PRT; 231 AA.  
AC Q9MJ64  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ORF18.  
OS Physarum polycephalum (Slime mold).  
OG Mitochondrion.  
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;  
OC Physarum.  
OX NCBI\_TaxID=5791;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takano H.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21080535; PubMed=11212908;  
RA Takano H., Abe T., Sakurai R., Moriyama Y., Miyazawa Y., Nozaki H.,  
Kawano S., Sasaki N., Kuroiwa T.;  
RT "The complete DNA sequence of the mitochondrial genome of Physarum  
polycephalum.";  
RL Mol. Gen. Genet. 264:539-545(2001).  
DR ENBL: AB027295; BAB08098.1; -  
KW Mitochondrion.  
SQ SEQUENCE 231 AA; 25949 MW; 0FD9ECD3A2058C0C CRC64;

Query Match 100.0%; Score 27; DB 8; Length 231;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5  
|||||  
Db 154 DYVIN 158

## RESULT 7

Q9R282 PRELIMINARY; PRT; 258 AA.  
AC Q9R282  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Spermine synthase (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129/SVJ;  
RA Korhonen V.P., Niiranen K., Halmekyto M., Pietila M., Diegelman P.,  
Parkkinen J.J., Eloranta T., Porter C.W., Alhonen L., Janne J.;  
RT "Spermine Deficiency Resulting from Targeted Disruption of the  
Spermine Synthase Gene in Embryonic Stem Cells Leads to Enhanced  
Sensitivity to Antiproliferative Drugs.";  
RL Mol. Pharmacol. 59:231-238(2001).  
DR ENBL: AF136179; AAD33057.1; -  
DR InterPro; IPR001045; Sprmine\_synthase.  
DR Pfam; PF01564; Spermine\_synth; 1.  
DR PROSITE; PS01330; SPERMIDINE\_SYNTHASE; 1.  
FT NON\_TER 1 258  
SQ SEQUENCE 258 AA; 29165 MW; 742A778011ACC8D2 CRC64;

Query Match 100.0%; Score 27; DB 11; Length 258;

```

Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 214 DYVIN 218
|||||

RESULT 8
Q9ROWO PRELIMINARY; PRT; 259 AA.
AC Q9ROWO
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TOU3.
GN TOU3 OR NNA2036.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RS SEQUENCE FROM N.A.
STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AF058689; AAF06687.1; -
DR EMBL; AL162757; CAB85255.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 259 AA; 29564 MW; FC2AD5234C6E4CBE CRC64;

Query Match 100.0%; Score 27; DB 16; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 78 DYVIN 82
|||||

RESULT 9
Q9I60 PRELIMINARY; PRT; 298 AA.
ID Q9I60
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Probable transcriptional regulator.
GN MLL2551.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OX Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RS SEQUENCE FROM N.A.
STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003000; BAB49656.1; -

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DR InterPro: IPR000847; HTH_LysR.
DR InterPro: IPR005119; LysR_subst.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 298 AA; 33459 MW; 2D9176927BEB7DE3 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 245 DYVIN 249
|||||

RESULT 10
Q98RF0 PRELIMINARY; PRT; 299 AA.
ID Q98RF0
AC Q98RF0
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Hypothetical protein MYP0_0590.
GN MYP0_0590.
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RS SEQUENCE FROM N.A.
STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445563; CAC13232.1; -
DR MYPULIST; MYP0_0590; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 299 AA; 35162 MW; F932B224FC7CC801 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 299;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5
DB 73 DYVIN 77
|||||

RESULT 11
Q9CG74 PRELIMINARY; PRT; 303 AA.
ID Q9CG74
AC Q9CG74
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE LysR family transcriptional regulator.
GN RLRA OR LL1236.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RS SEQUENCE FROM N.A.
STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauer S., Jaillon O., Malarne K.,

```

RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*  
 RT *lactis* ssp. *lactis* IIL1403.";  
 RL Genome Res. 11:731-753(2001).  
 CC 1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.  
 DR EMBL: AE006355; RAK05334.1; -;  
 DR InterPro: IPR000847; HTH\_LysR.  
 DR InterPro: IPR005119; LysR\_subst.  
 DR Pfam: PF00126; HTH\_1; 1.  
 DR Pfam: PF03466; LysR\_substrate; 1.  
 DR PRINTS: PR00039; HTHLYSR.  
 DR PROSITE: PS00044; HTH\_LYSR\_FAMILY; UNKNOWN1.  
 DR DNA-binding; Transcription regulation; Complete proteome.  
 KW  
 SQ SEQUENCE 303 AA; 34906 MW; 79FF10A56F6C8983 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 303;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||

Db 209 DYVIN 213

# RESULT 12

Q9HYI7 PRELIMINARY; PRT; 341 AA.

AC Q9HYI7  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Leucine dehydrogenase.  
 GN LDH OR PA3418.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 Raizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL: AE004763; AG06806.1; -;  
 DR InterPro: IPR001625; GLFV\_Dh.  
 DR InterPro: IPR000205; NAD\_binding.  
 DR Pfam: PF00208; GLFV\_dehydrog; 1.  
 DR Pfam: PF02812; GLFV\_dehydrog\_N; 1.  
 DR PRINTS: PR00082; GLFVHDRGNASE.  
 KW Complete proteome.  
 SQ SEQUENCE 341 AA; 35633 MW; ECCB810C13BF0B40 CRC64;

Query Match 100.0%; Score 27; DB 16; Length 341;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 277 DYVIN 281

# RESULT 13

Q9K7Z4 PRELIMINARY; PRT; 345 AA.

AC Q9K7Z4;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein BH3213.  
 GN BH3213.  
 OS *Bacillus halodurans*.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=86665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*  
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL: AP001518; BAB06932.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 345 AA; 38740 MW; 938F7707056F598E CRC64;

Query Match 100.0%; Score 27; DB 16; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYVIN 5

|||||

Db 144 DYVIN 148

# RESULT 14

Q96XE0 PRELIMINARY; PRT; 347 AA.

AC Q96XE0  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Putative alcohol dehydrogenase.  
 GN ST2577.  
 OS *Sulfolobus tokodaii*.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxID=111955;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;  
 RX PubMed=11572479;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,  
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
 RA Oshima T., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic thermoacidophilic  
 RT *Crenarchaeon*, *Sulfolobus tokodaii* strain 7.";  
 RL DNA Res. 8:123-140(2001).  
 DR EMBL: AP000950; BAB67688.1; -;  
 DR InterPro: IPR002328; ADH\_zinc.  
 DR InterPro: IPR002085; Adh\_zn\_family.  
 DR InterPro: IPR000051; SAM\_bind.  
 DR Pfam: PF00107; adh\_zinc; 1.  
 DR PROSITE: PS00059; ADH\_ZINC; UNKNOWN1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 347 AA; 37569 MW; 46059B8AE2382DF0 CRC64;

Query Match 100.0%; Score 27; DB 17; Length 347;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYVIN 5

|||||

Db 218 DYVIN 222

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RESULT 15
O58389
ID O58389 PRELIMINARY; PRT; 348 AA.
AC O58389;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 348AA long hypothetical dehydrogenase.
GN PH0655.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
DR EMBL; AP000003; BAA29746.1; -.
DR HSSP; P07846; ISDG.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR004627; Tdh.
DR Pfam; PF00107; adh_zinc; 1.
DR TIGRFAMs; TIGR00692; tdh; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; Complete proteome.
SQ SEQUENCE 348 AA; 37785 MW; 313F368AE83F793E CRC64;

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Query Match      100.0%; Score 27; DB 17; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DYVIN 5
DB 214 DYVIN 218

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Search completed: February 14, 2003, 11:18:36
time : 12.5699 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 46.0645 Seconds  
(without alignments)  
49.176 Million cell updates/sec

Title: US-09-701-001B-2  
Perfect score: 94  
Sequence: 1 E1YPCGSAYNEMFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
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- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 94    | 100.0       | 17     | 21 | AAV59257    |
| 2          | 94    | 100.0       | 17     | 21 | AAV51134    |
| 3          | 94    | 100.0       | 110    | 21 | AAV59262    |
| 4          | 94    | 100.0       | 110    | 21 | AAV51139    |
| 5          | 94    | 100.0       | 118    | 21 | AAV59266    |
| 6          | 94    | 100.0       | 118    | 21 | AAV51143    |
| 7          | 94    | 100.0       | 118    | 21 | AAV51145    |
| 8          | 94    | 100.0       | 305    | 21 | AAV59264    |
| 9          | 94    | 100.0       | 305    | 21 | AAV59265    |
| 10         | 94    | 100.0       | 305    | 21 | AAV51141    |

|    |    |       |     |    |          |                    |
|----|----|-------|-----|----|----------|--------------------|
| 11 | 94 | 100.0 | 305 | 21 | AAV51142 | Murine derived pro |
| 12 | 88 | 93.6  | 119 | 21 | AAV51264 | Monoclonal antibod |
| 13 | 88 | 93.6  | 137 | 14 | AAV32124 | Anti-CD4 antibody  |
| 14 | 81 | 86.2  | 121 | 18 | AAW07437 | Anti-DNA antibody  |
| 15 | 76 | 80.9  | 123 | 16 | AAW79877 | Anti-EGFR antibody |
| 16 | 73 | 77.7  | 113 | 18 | AAW04591 | Anti-DNA antibody  |
| 17 | 73 | 77.7  | 248 | 20 | AAV17960 | Mouse scfV fragmen |
| 18 | 73 | 77.7  | 248 | 20 | AAV17965 | Mouse scfV fragmen |
| 19 | 72 | 76.6  | 116 | 17 | AAW03742 | Murine monoclonal  |
| 20 | 71 | 75.5  | 355 | 18 | AAW35133 | R. pipiens recombi |
| 21 | 70 | 74.5  | 242 | 20 | AAV17959 | Mouse scfV fragmen |
| 22 | 70 | 74.5  | 242 | 20 | AAV17961 | Mouse scfV fragmen |
| 23 | 70 | 74.5  | 251 | 20 | AAV17958 | Mouse scfV fragmen |
| 24 | 70 | 74.5  | 251 | 20 | AAV17962 | Mouse scfV fragmen |
| 25 | 70 | 74.5  | 507 | 23 | AAU72858 | 8G7C10x4-7 bispec  |
| 26 | 70 | 74.5  | 510 | 23 | AAU72859 | 6E5A7x4-7 bispecif |
| 27 | 70 | 74.5  | 510 | 23 | AAU72860 | Human p53 tetramer |
| 28 | 70 | 74.5  | 532 | 21 | AAV78328 | Bispecific anti-ze |
| 29 | 68 | 72.3  | 91  | 18 | AAW18276 | PrP 24 antibody fr |
| 30 | 68 | 72.3  | 91  | 18 | AAW18267 | PrP 81 heavy chain |
| 31 | 68 | 72.3  | 91  | 20 | AAW85906 | PrP 81 heavy chain |
| 32 | 68 | 72.3  | 91  | 20 | AAW85914 | Amino acid sequenc |
| 33 | 68 | 72.3  | 91  | 22 | AAW65858 | Anti-PrP antibody  |
| 34 | 68 | 72.3  | 91  | 22 | AAW65866 | Anti-PrP antibody  |
| 35 | 68 | 72.3  | 91  | 23 | ABP51792 | Anti-prion protein |
| 36 | 68 | 72.3  | 91  | 23 | ABP51800 | Anti-prion protein |
| 37 | 68 | 72.3  | 92  | 18 | AAW18277 | PrP 26 antibody fr |
| 38 | 68 | 72.3  | 92  | 18 | AAW18284 | PrP 39 antibody fr |
| 39 | 68 | 72.3  | 92  | 20 | AAW85921 | Amino acid sequenc |
| 40 | 68 | 72.3  | 92  | 20 | AAW85915 | Amino acid sequenc |
| 41 | 68 | 72.3  | 92  | 22 | AAW65867 | Anti-PrP antibody  |
| 42 | 68 | 72.3  | 92  | 22 | AAW65873 | Anti-PrP antibody  |
| 43 | 68 | 72.3  | 92  | 23 | ABP51801 | Anti-prion protein |
| 44 | 68 | 72.3  | 92  | 23 | ABP51807 | Anti-prion protein |
| 45 | 68 | 72.3  | 95  | 18 | AAW18285 | PrP 40 antibody fr |

## ALIGNMENTS

RESULT 1  
AAV59257  
ID AAV59257 standard; peptide; 17 AA.  
XX AAV59257;  
XX AC  
XX DT 17-APR-2000 (first entry)  
XX Anticbody 4H5 H chain variable region CDR2 fragment.  
DE CD4 antigen: anti-human; antibody; 4H5; drug; CDR;  
KW complementarity determining region.  
OS Mus sp.  
XX JP11332563-A.  
PN 07-DEC-1999.  
XX 26-MAY-1998; 98JP-0163034.  
XX 26-MAY-1998; 98JP-0163034.  
XX (ASAH ) ASAH KASEI KOGYO KK.  
XX WPI; 2000-091351/08.  
XX An antibody and the nucleic acid coding the antibody -  
XX Claim 1; Page 14; 25pp; Japanese.  
XX The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and

CC application for drugs. It is highly safe in human dose. Sequences  
 CC AAY59256-58 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the H chain variable region of the  
 CC antibody 4H5 respectively.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17  
 |||||  
 Db 1 EYPGSGSAYYNEMFKG 17

RESULT 2  
 AAY51134  
 ID AAY51134 standard; Protein; 17 AA.  
 XX  
 AC AAY51134;

31-MAR-2000 (first entry)

DE Murine CD4/CD34 recognizing antibody heavy chain CDR-2 region #1.

XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; complementarity determining region;  
 KW CDR-2; heavy chain; murine.

XX Mus sp.

OS WO9961629-A1.

PN 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH) KASEI KOGYO KK.

PA (ASAH) ASAHI MEDICAL CO LTD.

PI Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 the separation of CD4 or CD34 positive cells -

PS Claim 3; Page 76; 11ipp; Japanese.

XX This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived complementarity determining  
 CC region CDR-2 protein fragment which is used to illustrate the method of  
 CC the invention.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17

Db 1 EYPGSGSAYYNEMFKG 17  
 |||||

RESULT 3  
 AAY59262  
 ID AAY59262 standard; protein; 110 AA.  
 XX  
 AC AAY59262;  
 XX 17-APR-2000 (first entry)  
 DT  
 DE Antibody 4H5 H chain variable region.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.

OS Mus sp.

XX JPI1332563-A.

PN 07-DEC-1999.

XX 26-MAY-1998; 98JP-0163034.

XX 26-MAY-1998; 98JP-0163034.

XX (ASAH) KASEI KOGYO KK.

XX WPI; 2000-091351/08.

XX N-PSDB; AAZ58661.

XX An antibody and the nucleic acid coding the antibody -

XX Claim 5; Page 15; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain variable region of the antibody 4H5.

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 94; DB 21; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEMFKG 17  
 |||||  
 Db 42 EYPGSGSAYYNEMFKG 58

RESULT 4  
 AAY51139  
 ID AAY51139 standard; Protein; 110 AA.

XX AAY51139;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #1.

XX Cluster differentiation; cell separation; antibody; CD4; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

*pcr priority for instant*

PR 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 XX (ASAH ) ASahi KASEI KOGYO KK.  
 PA (ASAH ) ASahi MEDICAL CO LTD.  
 XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 DR WPI; 2000-086720/07.  
 DR N-PSDB; AA244203.  
 XX  
 XX  
 PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 PS Claim 22; Page 78; 111pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 SQ Sequence 110 AA;  
 Query Match 100.0%; Score 94; DB 21; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIYPGSGSAYYNEMFKG 17  
 DB 42 EIYPGSGSAYYNEMFKG 58  
 RESULT 5  
 AAY59266  
 ID AAY59266 standard; protein; 118 AA.  
 AC  
 XX  
 XX  
 DT 17-APR-2000 (first entry)  
 VT Antibody 4H5 H chain fragment.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 DR N-PSDB; AA258689.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 XX  
 PS Disclosure; Page 22; 25pp; Japanese.  
 XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents a H chain fragment of the antibody 4H5.

XX  
 SQ Sequence 118 AA;  
 Query Match 100.0%; Score 94; DB 21; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIYPGSGSAYYNEMFKG 17  
 DB 50 EIYPGSGSAYYNEMFKG 66  
 RESULT 6  
 AAY51143  
 ID AAY51143 standard; Protein; 118 AA.  
 AC  
 XX  
 AC AAY51143;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 DE Murine derived protein fragment #5.  
 XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9961629-A1.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 24-MAY-1999; 99WO-JP02711.  
 XX  
 PR 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 XX  
 PA (ASAH ) ASahi KASEI KOGYO KK.  
 PA (ASAH ) ASahi MEDICAL CO LTD.  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX  
 DR WPI; 2000-086720/07.  
 XX  
 PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 PS Disclosure; Page 94-95; 111pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 SQ Sequence 118 AA;  
 Query Match 100.0%; Score 94; DB 21; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIYPGSGSAYYNEMFKG 17  
 DB 50 EIYPGSGSAYYNEMFKG 66  
 RESULT 7  
 AAY51145

ID AAY51145 standard; Protein; 118 AA.  
XX AC AAY51145;  
XX DT 31-MAR-2000 (first entry)  
XX DE Murine derived protein fragment #7.  
XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hemopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.  
XX OS Mus sp.  
XX PN WO9961629-A1.  
XX PD 02-DEC-1999.  
XX PF 24-MAY-1999; 99WO-JP02711.  
XX PR 25-MAY-1998; 98JP-0159957.  
XX 26-MAY-1998; 98JP-0163023.  
XX (ASAH ) ASAH KASEI KOGYO KK.  
XX PA (ASAH ) ASAH MEDICAL CO LTD.  
XX PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX WPI; 2000-086720/07.  
XX DR N-PSDB; AAZ44231.  
XX PT Devices containing antibodies recognising CD4 or CD34 and their use for  
XX the separation of CD4 or CD34 positive cells -  
XX PS Disclosure; Page 96-97; 111pp; Japanese.  
XX CC This invention describes a novel device (I) for separating cluster  
XX differentiation (CD)-positive cells using a recombinant (chimeric or  
XX single-chain) antibody recognising CD4 or CD34. The devices are useful  
XX for the separation of CD4 or CD34 positive cells, which is useful for  
XX the collection of hematopoietic undifferentiated cells, elimination of  
XX lymphocytes from cells to be used in bone marrow transplantation, the  
XX detection of leukemic cells and the production of medicinal  
XX compositions for the treatment of HIV infection and autoimmune diseases.  
XX CC This sequence represents a murine derived protein fragment which is used  
XX to illustrate the method of the invention.  
XX SQ Sequence 118 AA;

Query Match 100.0%; Score 94; DB 21; Length 118;  
Best Local Similarity 100.0%; Pred. No. 3.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYFGSGSAYYNEMFKG 17  
|||  
Db 50 EYFGSGSAYYNEMFKG 66

RESULT 8  
AAY59264  
ID AAY59264 standard; protein; 305 AA.  
XX AC AAY59264;  
XX DT 17-APR-2000 (first entry)  
XX DE Antibody 4H5 H chain sequence.  
XX KW CD4 antigen; anti-human; antibody; 4H5; drug.  
XX OS Mus sp.  
XX PN JP11332563-A.

XX PD 07-DEC-1999.  
XX PF 26-MAY-1998; 98JP-0163034.  
XX PR 26-MAY-1998; 98JP-0163034.  
XX PA (ASAH ) ASAH KASEI KOGYO KK.  
XX WPI; 2000-091351/08.  
XX DR N-PSDB; AAZ58663.  
XX PT An antibody and the nucleic acid coding the antibody -  
XX PS Disclosure; Page 16-17; 25pp; Japanese.  
XX CC The invention provides an antibody having affinity to CD4 antigen. The  
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and  
XX application for drugs. It is highly safe in human dose. The present  
XX sequence represents the H chain sequence of the antibody 4H5.  
XX SQ Sequence 305 AA;

Query Match 100.0%; Score 94; DB 21; Length 305;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYFGSGSAYYNEMFKG 17  
|||  
Db 198 EYFGSGSAYYNEMFKG 214

RESULT 9  
AAY59265  
ID AAY59265 standard; protein; 305 AA.  
XX AC AAY59265;  
XX DT 17-APR-2000 (first entry)  
XX DE Antibody 4H5 L chain sequence.  
XX KW CD4 antigen; anti-human; antibody; 4H5; drug.  
XX OS Mus sp.  
XX PN JP11332563-A.

SQ Sequence 118 AA;

Query Match 100.0%; Score 94; DB 21; Length 305;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYFGSGSAYYNEMFKG 17  
|||  
Db 198 EYFGSGSAYYNEMFKG 214

RESULT 9

Query Match 100.0%; Score 94; DB 21; Length 305;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 EYPGSGSAYNEMFKG 17  
DB 72 EYPGSGSAYNEMFKG 88  
RESULT 10  
AAAY51141  
ID AAY51141 standard; Protein; 305 AA.  
XX AC AAY51141;  
XX DT 31-MAR-2000 (first entry)  
XX DE Murine derived protein fragment #3.  
XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
XX hemapopietic; undifferentiated; lymphocyte; bone marrow transplantation;  
XX HIV infection; autoimmune disease; murine.  
XX OS Mus sp.  
XX PN WO9961629-A1.  
XX PD 02-DEC-1999.  
XX PF 24-MAY-1999; 99WO-JP02711.  
XX PR 25-MAY-1998; 98JP-0159957.  
XX PR 26-MAY-1998; 98JP-0163023.  
XX PA (ASAH ) ASAH KASEI KOGYO KK.  
XX PA (ASAH ) ASAH MEDICAL CO LTD.  
XX PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX WPI; 2000-086720/07.  
XX DR N-PSDB; AAZ44205.  
XX PT Devices containing antibodies recognising CD4 or CD34 and their use for  
XX the separation of CD4 or CD34 positive cells -  
XX PS Claim 22; Page 80-82; 11lpp; Japanese.  
XX CC This invention describes a novel device (I) for separating cluster  
XX differentiation (CD)-positive cells using a recombinant (chimeric or  
XX single-chain) antibody recognising CD4 or CD34. The devices are useful  
XX for the separation of CD4 or CD34 positive cells, which is useful for  
XX the collection of hematopoietic undifferentiated cells, elimination of  
XX lymphocytes from cells to be used in bone marrow transplantation, the  
XX detection of leukemic cells and the production of medicinal  
XX compositions for the treatment of HIV infection and autoimmune diseases.  
XX CC This sequence represents a murine derived protein fragment which is used  
XX to illustrate the method of the invention.  
XX SQ Sequence 305 AA;  
Query Match 100.0%; Score 94; DB 21; Length 305;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYPGSGSAYNEMFKG 17  
DB 198 EYPGSGSAYNEMFKG 214  
RESULT 11  
AAAY51142  
ID AAY51142 standard; Protein; 305 AA.  
XX AC AAY51142;  
XX DT 31-MAR-2000 (first entry)

XX Murine derived protein fragment #4.  
XX DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
XX KW hemapopietic; undifferentiated; lymphocyte; bone marrow transplantation;  
XX KW HIV infection; autoimmune disease; murine.  
XX OS Mus sp.  
XX PN WO9961629-A1.  
XX PD 02-DEC-1999.  
XX PF 24-MAY-1999; 99WO-JP02711.  
XX PR 25-MAY-1998; 98JP-0159957.  
XX PR 26-MAY-1998; 98JP-0163023.  
XX PA (ASAH ) ASAH KASEI KOGYO KK.  
XX PA (ASAH ) ASAH MEDICAL CO LTD.  
XX PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX WPI; 2000-086720/07.  
XX DR N-PSDB; AAZ44205.  
XX PT Devices containing antibodies recognising CD4 or CD34 and their use for  
XX the separation of CD4 or CD34 positive cells -  
XX PS Claim 22; Page 82-84; 11lpp; Japanese.  
XX CC This invention describes a novel device (I) for separating cluster  
XX differentiation (CD)-positive cells using a recombinant (chimeric or  
XX single-chain) antibody recognising CD4 or CD34. The devices are useful  
XX for the separation of CD4 or CD34 positive cells, which is useful for  
XX the collection of hematopoietic undifferentiated cells, elimination of  
XX lymphocytes from cells to be used in bone marrow transplantation, the  
XX detection of leukemic cells and the production of medicinal  
XX compositions for the treatment of HIV infection and autoimmune diseases.  
XX CC This sequence represents a murine derived protein fragment which is used  
XX to illustrate the method of the invention.  
XX SQ Sequence 305 AA;  
Query Match 100.0%; Score 94; DB 21; Length 305;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYPGSGSAYNEMFKG 17  
DB 72 EYPGSGSAYNEMFKG 88  
RESULT 12  
AAAY51264  
ID AAY51264 standard; peptide; 119 AA.  
XX AC AAY51264;  
XX DT 14-APR-2000 (first entry)  
XX DE Monoclonal antibody MAK CD4 heavy chain variable region peptide.  
XX KW Framework region; monoclonal antibody; variable domain; detection;  
XX KW immunotherapy; MAK CD4.  
XX OS Unidentified.  
XX PN DE19828466-A1.  
XX PR 30-DEC-1999.  
XX PD 26-JUN-1998; 98DE-1028466.  
XX PF

*PCT priority for instant*

*PCT priority for instant*

*not a perfect match*

|           |  |
|-----------|--|
| XX        | Claim 5; Page 12; 18pp; German.                                      |
| XX        | This sequence is the heavy chain variable region of a preferred      |
| XX        | anti-CD4 monoclonal antibody for use in the claimed synergistic      |
| CC        | composition. Mab WT 3.10 is deposited as clone 3.101/SB10 (ECACC     |
| CC        | 90090702). The anti-CD4 antibody is used with at least one anti-IL2R |
| CC        | alpha or beta antibody. Individually the antibodies are strongly     |
| CC        | inhibiting and when used together their immunosuppressive properties |
| CC        | are improved; they synergistically inhibit T-helper cell             |
| CC        | proliferation to effectively inhibit transplant rejection at low     |
| CC        | doses without significantly reducing the general immune response.    |
| CC        | See also AAQ36608-Q36616.  |
| XX        |  |
| XX        | Sequence 137 AA;   |
| SQ        |  |
|           | Query Match 93.6%; Score 88; DB 14; Length 137;                      |
|           | Best Local Similarity 94.1%; Pred. No. 3.1e-05;                      |
|           | Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps             |
| OY        | 1 EIYPGSGSAYNEMFKG 17  |
|           |  |
| Db        | 68 EIYPGSGSAYNEKFKG 84   |
|           |  |
| RESULT 14 |  |
| AAW07437  |  |
| ID        | AAW07437 standard; Protein; 121 AA.                                  |
| XX        | AAW07437;  |
| XX        |  |
| DT        | 12-AUG-1997 (first entry)  |
| DE        | Anti-DNA antibody 4b2 group heavy chain variable region.             |
| XX        |  |
| KW        | Heavy chain; variable region; anti-DNA; monoclonal; antibody;        |
| KW        | 4b2 group; hairpin; diagnosis; inflammatory glomerulonephritis;      |
| KW        | systemic lupus erythematosus; screening; treatment; prevention;      |
| KW        | SLF; disease; consensus; putative.                                   |
| XX        |  |
| OS        | Synthetic.   |
| XX        |  |
| Key       | Location/Qualifiers  |
| FF        | 1..30  |
| FT        | /label= framework_I  |
| FT        | 31..35   |
| FT        | /label= CDR_I  |
| FT        | 36..49   |
| FT        | /label= framework_II   |
| FT        | 50..66   |
| FT        | /label= CDR_II   |
| FT        | 67..98   |
| FT        | /label= framework_III  |
| FT        | 99..110  |
| FT        | /label= CDR_III  |
| FT        | 111..121   |
| FT        | /label= J_region   |
| XX        |  |
| PN        | WO9636361-A1.  |
| XX        |  |
| PD        | 21-NOV-1996.   |
| XX        |  |
| PF        | 16-MAY-1996; 96WO-US07113.   |
| XX        |  |
| PR        | 18-MAY-1995; 95US-0443540.   |
| XX        |  |
| PA        | (UNMI ) UNIV MICHIGAN.   |
| XX        |  |
| PI        | Glick GD, Swanson PC;  |
| XX        |  |
| DR        | WPI; 1997-011854/01.   |
| XX        |  |
| XX        | N-PSDB; AAT43806.  |

PT Anti-DNA antibody which specifically binds DNA hairpin - useful to  
 PT develop prods. for diagnosis and treatment of disorders, e.g.  
 PT glomerulonephritis or systemic lupus erythematosus  
 XX Example; Fig 9; 102pp; English.

PS  
 CC The present sequence is the heavy chain variable region of the  
 CC group 4b2 putative consensus anti-DNA monoclonal antibody (Mab),  
 CC which has a high affinity for single stranded DNA, low or no  
 CC affinity for double stranded DNA and specifically binds a DNA  
 CC hairpin. The Mab can be used to diagnose disorders associated with the  
 CC pathological complexation of DNA, e.g. inflammatory  
 CC glomerulonephritis and systemic lupus erythematosus. It can also be  
 CC used to generate reagents to screen for pharmaceutical agents, and  
 CC treat and/or prevent an above disorder.  
 CC The sequence was derived by aligning homologous anti-DNA Mab,  
 CC whose sequences have been published, as well as several Mab of  
 CC other specificities obtained from a database search.

Sequence 121 AA;

Query Match 86.2%; Score 81; DB 18; Length 121;  
 Best Local Similarity 82.4%; Pred. No. 0.00028;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYINEMFKG 17  
 |||||: |||| |||  
 Db 50 EIYPGSGNTYINEMFKG 66

RESULT 15

AAR79877  
 ID AAR79877 standard; Protein; 123 AA.

XX  
 AC AAR79877;

XX 24-MAY-1996 (first entry)

XX Anti-EGFR antibody heavy chain variable region (Clone L2 1C).

XX Single chain antibody; antibody; epidermal growth factor receptor;  
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;  
 KW assessment; phage antibody library.

XX Mus musculus.

| Key             | Location/Qualifiers         |
|-----------------|-----------------------------|
| Region 1..30    | /label= Framework region 1. |
| Region 31..35   | /label= CDR1.               |
| Region 36..49   | /label= Framework region 2. |
| Region 50..66   | /label= CDR2.               |
| Region 67..98   | /label= Framework region 3. |
| Region 99..112  | /label= CDR3.               |
| Region 113..123 | /label= Framework region 4. |

XX WO9525167-A1.

XX 21-SEP-1995.

XX 16-MAR-1995; 95WO-EP00978.

XX 02-DEC-1994; 94EP-0118970.

XX 17-MAR-1994; 94EP-0104160.

XX (MERE ) MERCK PATENT GMBH.

XX

PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;  
 PI Kettleborough AC, Mitjans F, Piulats J, Rosell E;  
 XX WPI; 1995-336972/43.

XX Anti-EGFR antibodies and single chain Fv antibody fragments -  
 PT obtained from phage-antibody libraries, useful for diagnosis and  
 PT therapy of tumours

XX Disclosure; Figure 1A; 93pp; English.

XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
 CC and antibodies constructed from anti-EGFR antibody fragments can be  
 CC used for diagnosis of tumours and assessment of tumour growth in  
 CC vitro and in vivo. They may also be used in a pharmaceutical  
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
 CC The antibodies and fragments are derived from mice but are humanised  
 CC so as to cause minimum reaction against them. They are produced  
 CC using the phage antibody library. (See AAT04011-T04026 and  
 CC AAR79858-R79873)

XX Sequence 123 AA;

Query Match 80.9%; Score 76; DB 16; Length 123;  
 Best Local Similarity 81.2%; Pred. No. 0.0015;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGSAYINEMFKG 17  
 |||||: |||| |||  
 Db 51 IYPGNGSTYINEMFKG 66

Search completed: February 14, 2003, 11:15:42

Job time : 47.0645 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 : Search time 15.3548 Seconds  
(without alignments)  
32.575 Million cell updates/sec

Title: US-09-701-001B-2  
Perfect score: 94  
Sequence: 1 EIYPGSGSAYNEMFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description       |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1          | 88    | 93.6        | 119    | 4 US-09-344-587-11  | Sequence 11, Appl |
| 2          | 81    | 86.2        | 98     | 3 US-08-881-037-64  | Sequence 64, Appl |
| 3          | 73    | 77.7        | 113    | 3 US-08-881-037-18  | Sequence 18, Appl |
| 4          | 73    | 77.7        | 121    | 3 US-08-881-037-65  | Sequence 65, Appl |
| 5          | 71    | 75.5        | 355    | 3 US-08-875-811-57  | Sequence 57, Appl |
| 6          | 68    | 72.3        | 91     | 2 US-08-713-939A-70 | Sequence 70, Appl |
| 7          | 68    | 72.3        | 91     | 2 US-08-713-939A-78 | Sequence 78, Appl |
| 8          | 68    | 72.3        | 91     | 4 US-09-036-579-70  | Sequence 70, Appl |
| 9          | 68    | 72.3        | 91     | 4 US-09-036-579-78  | Sequence 78, Appl |
| 10         | 68    | 72.3        | 91     | 4 US-09-550-374-70  | Sequence 70, Appl |
| 11         | 68    | 72.3        | 91     | 4 US-09-550-374-78  | Sequence 78, Appl |
| 12         | 68    | 72.3        | 92     | 2 US-08-713-939A-79 | Sequence 79, Appl |
| 13         | 68    | 72.3        | 92     | 2 US-08-713-939A-85 | Sequence 85, Appl |
| 14         | 68    | 72.3        | 92     | 4 US-09-036-579-79  | Sequence 79, Appl |
| 15         | 68    | 72.3        | 92     | 4 US-09-036-579-85  | Sequence 85, Appl |
| 16         | 68    | 72.3        | 92     | 4 US-09-550-374-79  | Sequence 79, Appl |
| 17         | 68    | 72.3        | 92     | 4 US-09-550-374-85  | Sequence 85, Appl |
| 18         | 68    | 72.3        | 95     | 2 US-08-713-939A-86 | Sequence 86, Appl |
| 19         | 68    | 72.3        | 95     | 4 US-09-036-579-86  | Sequence 86, Appl |
| 20         | 68    | 72.3        | 95     | 4 US-09-550-374-86  | Sequence 86, Appl |
| 21         | 68    | 72.3        | 101    | 2 US-08-713-939A-82 | Sequence 82, Appl |
| 22         | 68    | 72.3        | 101    | 4 US-09-036-579-82  | Sequence 82, Appl |
| 23         | 68    | 72.3        | 101    | 4 US-09-550-374-82  | Sequence 82, Appl |
| 24         | 68    | 72.3        | 103    | 2 US-08-713-939A-84 | Sequence 84, Appl |
| 25         | 68    | 72.3        | 103    | 4 US-09-036-579-84  | Sequence 84, Appl |
| 26         | 68    | 72.3        | 103    | 4 US-09-550-374-84  | Sequence 84, Appl |
| 27         | 68    | 72.3        | 108    | 2 US-08-713-939A-83 | Sequence 83, Appl |

28 68 72.3 108 4 US-09-036-579-83 Sequence 83, Appl  
29 68 72.3 108 4 US-09-550-374-83 Sequence 83, Appl  
30 68 72.3 114 2 US-08-713-939A-68 Sequence 68, Appl  
31 68 72.3 114 2 US-08-713-939A-76 Sequence 76, Appl  
32 68 72.3 114 2 US-08-713-939A-77 Sequence 77, Appl  
33 68 72.3 114 4 US-09-036-579-68 Sequence 68, Appl  
34 68 72.3 114 4 US-09-036-579-76 Sequence 76, Appl  
35 68 72.3 114 4 US-09-036-579-77 Sequence 77, Appl  
36 68 72.3 114 4 US-09-550-374-68 Sequence 68, Appl  
37 68 72.3 114 4 US-09-550-374-76 Sequence 76, Appl  
38 68 72.3 114 4 US-09-550-374-77 Sequence 77, Appl  
39 67 71.3 119 3 US-08-767-128-20 Sequence 20, Appl  
40 66 70.2 116 2 US-08-888-366-2 Sequence 2, Appl  
41 66 70.2 117 4 US-09-344-587-12 Sequence 12, Appl  
42 66 70.2 119 1 US-08-458-516-10 Sequence 10, Appl  
43 66 70.2 119 1 US-08-458-516-11 Sequence 11, Appl  
44 66 70.2 138 1 US-08-458-516-7 Sequence 7, Appl  
45 66 70.2 222 1 US-08-458-516-22 Sequence 22, Appl

## ALIGNMENTS

RESULT 1  
US-09-344-587-11  
; Sequence 11, Application US/09344587  
; Patent No. 6331402  
; GENERAL INFORMATION:  
; APPLICANT: Praast, Gerald  
; APPLICANT: Nussbaum, Sabine  
; APPLICANT: Moessner, Ellen  
; APPLICANT: Lenz, Helmut  
; TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNOASSAYS BY SUBSTANCES  
; TITLE OF INVENTION: DERIVED FROM THE FRAMEWORK REGIONS OF ANTIBODIES  
; FILE REFERENCE: BMID 9928 4897/00/US-Im  
; CURRENT APPLICATION NUMBER: US/09/344,587  
; CURRENT FILING DATE: 1999-06-25  
; EARLIER APPLICATION NUMBER: DE 19828466.7  
; EARLIER FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 119  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-344-587-11

Query Match 93.6%; Score 88; DB 4; Length 119;  
Best Local Similarity 94.1%; Pred. No. 7e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYNEMFKG 17  
|||||  
Db 50 EIYPGSGSAYNEMFKG 66

RESULT 2  
US-08-881-037-64  
; Sequence 64, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-64

Query Match 86.2%; Score 81; DB 3; Length 98;  
Best Local Similarity 82.4%; Pred. No. 6e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
|||||: |||||  
DB 50 EIYPGSGNTYNEKFKG 66

RESULT 3  
US-08-881-037-18  
Sequence 18, Application US/08881037  
Patent No. 6080588  
GENERAL INFORMATION:  
APPLICANT: Klick, Gary D.  
APPLICANT: Swanson, Patrick C.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792

TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-18

Query Match 77.7%; Score 73; DB 3; Length 113;  
Best Local Similarity 76.5%; Pred. No. 0.00099;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
|||||: |||||  
DB 42 EIYPGSGNTYNEKFKG 58

RESULT 4  
US-08-881-037-65  
Sequence 65, Application US/08881037  
Patent No. 6080588  
GENERAL INFORMATION:  
APPLICANT: Klick, Gary D.  
APPLICANT: Swanson, Patrick C.  
TITLE OF INVENTION: DNA BINDING ANTIBODIES  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/881,037  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/443,540  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanski, Antoinette F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 203442110710  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX:  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-881-037-65

Query Match 77.7%; Score 73; DB 3; Length 121;  
Best Local Similarity 76.5%; Pred. No. 0.0011;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
|||||: |||||  
DB 50 EIYPGSGNTYNEKFKG 66

RESULT 5

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us-09-701-001b-2.raii

US-08-875-811-57  
; Sequence 57, Application US/08875811

: Sequence 57, Application US/08875811  
 : Patent No. 6045793  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Rybak, Susanna M.  
 : APPLICANT: Newton, Dianne L.  
 : APPLICANT: Boque, Lluís  
 : APPLICANT: Wlodawer, Alexander  
 :  
 : TITLE OF INVENTION: Recombinant Ribonuclease Proteins  
 :  
 : NUMBER OF SEQUENCES: 64  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend and Crew LLP  
 : STREET: Two Embarcadero Center, Eighth Floor  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94111-3834

ZIP: 94111-5624  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875.811  
FILING DATE: 19-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/02588

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US97/02588  
 FILING DATE: 19-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/011,800  
 FILING DATE: 21-FEB-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Faris, Susan K.  
 REGISTRATION NUMBER: 41,739  
 REFERENCE/DOCKET NUMBER: 015280-244100US  
 TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
08-875-811-57

Query Match 75.5%; Score 71; DB 3; Length 355;  
Best Local Similarity 70.6%; Pred. NO. 0.0062;  
Matches 12; Conservative 2; Mismatches 3; Indels

QY 1 EIYPGSGSAYYNEMFKG 17  
:|||||:|||||||  
Db 168 DIYPGSDNTYYNEKFKG 184

```

RESULT 6
US-08-713-939A-70
; Sequence 70, Application US/08713939A
; Patent No. 5846533
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; APPLICANT: Williamson, R. Anthony
; APPLICANT: Burcon, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPI
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
TELEX:
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-70

```

Query Match 72.3%; Score 68; DB 2; Length 91;  
Best Local Similarity 70.6%; Pred. No. 0.0042;  
Matches 12: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
||:| ||: ||| |||  
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 7  
US-08-713-939A-78  
: Sequence 78, Application US/08/713939A  
: Patent No. 5846533  
: GENERAL INFORMATION:  
: APPLICANT: Prusiner, Stanley B.  
: APPLICANT: Williamson, R. Anthony  
: APPLICANT: Burton, Dennis R.  
: TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
: NUMBER OF SEQUENCES: 86  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Fish & Richardson P.C.  
: STREET: 2200 Sand Hill Road  
: CITY: Menlo Park  
: STATE: CA  
: COUNTRY: U.S.A.  
: ZIP: 94025  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette  
: COMPUTER: IBM Compatible  
: OPERATING SYSTEM: DOS  
: SOFTWARE: FastSEQ Version 2.0  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/713, 939A  
: FILING DATE: 13-SEP-1996  
: CLASSIFICATION: 436  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Bozicevic, Karl  
: REGISTRATION NUMBER: 28,807  
: REFERENCE/DOCKET NUMBER: 06510/059001  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 415-854-5277





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Fri Feb 14 15:00:50 2003

TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-550-374-78

Query Match 72.3% Score 68; DB 4; Length 91;  
Best Local Similarity 70.6%; Pred. No. 0.0042;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVPGSGSAYYNEFKG 17  
Db 24 EIVPRSGNTYYNEFKG 40

RESULT 12  
US-08-713-939A-79  
Sequence 79, Application US/08713939A  
Patent No. 5846533  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
APPLICANT: Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713.939A  
FILING DATE: 13-SEP-1996  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-713-939A-79

Query Match 72.3% Score 68; DB 2; Length 92;  
Best Local Similarity 70.6%; Pred. No. 0.0043;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVPGSGSAYYNEFKG 17  
Db 24 EIVPRSGNTYYNEFKG 40

ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/550,374  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/036,579  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX:  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-550-374-70

Query Match 72.3% Score 68; DB 4; Length 91;  
Best Local Similarity 70.6%; Pred. No. 0.0042;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIVPGSGSAYYNEFKG 17  
Db 24 EIVPRSGNTYYNEFKG 40

RESULT 11  
US-09-550-374-78  
Sequence 78, Application US/09550374  
Patent No. 6372214  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
APPLICANT: Williamson, R. Anthony  
APPLICANT: Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/550,374  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/036,579  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:

Db 25 EIWPMSGNTYNEKPKG 41

## RESULT 13

US-08-713-939A-85  
; Sequence 85, Application US/08713939A  
; Patent No. 5846533  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley B.  
; APPLICANT: Williamson, R. Anthony  
; APPLICANT: Burton, Dennis R.  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 2200 Sand Hill Road  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94025

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,939A  
; FILING DATE: 13-SEP-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bozicevic, Karl  
; REGISTRATION NUMBER: 28,807  
; REFERENCE/DOCKET NUMBER: 06510/059001  
; TELEPHONE: 415-854-5277  
; TELEFAX: 415-854-0875  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-713-939A-85

Query Match 72.3%; Score 68; DB 2; Length 92;  
Best Local Similarity 70.6%; Pred. No. 0.0043;  
Matches 12; Conservative 2; Mismatches 3; Indels 0;

QY 1 EIYPGSGSAYYNEKPKG 17  
||: ||: ||| |||  
Db 25 EIWPMSGNTYNEKPKG 41

## RESULT 14

US-09-036-579-79  
; Sequence 79, Application US/09036579  
; Patent No. 6290954  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley B.  
; APPLICANT: Williamson, R. Anthony  
; APPLICANT: Burton, Dennis R.  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 2200 Sand Hill Road  
; CITY: Menlo Park  
; STATE: CA

; COUNTRY: U.S.A.  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,579  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/713,939  
; FILING DATE: 13-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bozicevic, Karl  
; REGISTRATION NUMBER: 28,807  
; REFERENCE/DOCKET NUMBER: 06510/059001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-5277  
; TELEFAX: 415-854-0875  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-036-579-79

Query Match 72.3%; Score 68; DB 4; Length 92;  
Best Local Similarity 70.6%; Pred. No. 0.0043;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEKPKG 17  
||: ||: ||| |||  
Db 25 EIWPMSGNTYNEKPKG 41

## RESULT 15

US-09-036-579-85  
; Sequence 85, Application US/09036579  
; Patent No. 6290954  
; GENERAL INFORMATION:  
; APPLICANT: Prusiner, Stanley B.  
; APPLICANT: Williamson, R. Anthony  
; APPLICANT: Burton, Dennis R.  
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 2200 Sand Hill Road  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,579  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/713,939  
; FILING DATE: 13-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bozicevic, Karl  
; REGISTRATION NUMBER: 28,807  
; REFERENCE/DOCKET NUMBER: 06510/059001

us-09-701-001b-2.ra

Fri Feb 14 15:00:50 2003

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-854-5277  
 TELEFAX: 415-854-0875  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 92 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-036-579-85

Query Match 72.3%; Score 68; DB 4; Length 92;  
 Best Local Similarity 70.6%; Pred. No. 0.0043;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 EIYPGSGSAYYNEMFKG 17  
 ||| ||: |||| |||  
 25 EIWPRSGNTYYNEMFKG 41

Search completed: February 14, 2003, 11:20:47  
 Job time : 15.3548 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 9,87097 Seconds  
(without alignments)  
44.001 Million cell updates/sec

Title: US-09-701-001b-2

Perfect score: 94

Sequence: 1 EIIYPGSGSAYNEMFKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Matched: 140259 seqs, 25548876 residues -

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pap.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pap.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 68    | 72.3        | 91     | 10    | US-09-943-906-70  |
| 2          | 68    | 72.3        | 91     | 10    | US-09-943-906-78  |
| 3          | 68    | 72.3        | 92     | 10    | US-09-943-906-79  |
| 4          | 68    | 72.3        | 92     | 10    | US-09-943-906-85  |
| 5          | 68    | 72.3        | 95     | 10    | US-09-943-906-86  |
| 6          | 68    | 72.3        | 101    | 10    | US-09-943-906-82  |
| 7          | 68    | 72.3        | 103    | 10    | US-09-943-906-84  |
| 8          | 68    | 72.3        | 108    | 10    | US-09-943-906-83  |
| 9          | 68    | 72.3        | 114    | 10    | US-09-943-906-68  |
| 10         | 68    | 72.3        | 114    | 10    | US-09-943-906-76  |
| 11         | 68    | 72.3        | 114    | 10    | US-09-943-906-77  |
| 12         | 66    | 70.2        | 117    | 9     | US-09-144-886-71  |
| 13         | 66    | 70.2        | 138    | 1     | US-08-779-784-31  |
| 14         | 65    | 69.1        | 17     | 10    | US-09-861-294-15  |
| 15         | 65    | 69.1        | 153    | 10    | US-09-861-294-4   |
| 16         | 64    | 68.1        | 105    | 10    | US-09-943-906-75  |
| 17         | 64    | 68.1        | 114    | 10    | US-09-943-906-69  |
| 18         | 62    | 66.0        | 31     | 9     | US-09-956-206A-31 |
| 19         | 62    | 66.0        | 91     | 10    | US-09-943-906-71  |

|    |      |     |    |                  |                   |
|----|------|-----|----|------------------|-------------------|
| 62 | 66.0 | 91  | 10 | US-09-943-906-81 | Sequence 81, Appl |
| 62 | 66.0 | 99  | 10 | US-09-943-906-80 | Sequence 80, Appl |
| 62 | 66.0 | 119 | 10 | US-09-839-447A-1 | Sequence 1, Appl  |
| 62 | 66.0 | 139 | 12 | US-10-006-773-13 | Sequence 13, Appl |
| 60 | 63.8 | 140 | 9  | US-09-905-928-6  | Sequence 6, Appl  |
| 59 | 62.8 | 117 | 9  | US-09-144-886-72 | Sequence 72, Appl |
| 59 | 62.8 | 515 | 10 | US-09-825-012-66 | Sequence 66, Appl |
| 59 | 62.8 | 517 | 10 | US-09-825-012-38 | Sequence 38, Appl |
| 59 | 62.8 | 519 | 10 | US-09-825-012-76 | Sequence 76, Appl |
| 59 | 62.8 | 519 | 10 | US-09-825-012-80 | Sequence 80, Appl |
| 59 | 62.8 | 521 | 10 | US-09-825-012-71 | Sequence 71, Appl |
| 59 | 62.8 | 525 | 10 | US-09-825-012-85 | Sequence 85, Appl |
| 59 | 62.8 | 527 | 10 | US-09-825-012-43 | Sequence 43, Appl |
| 59 | 62.8 | 529 | 10 | US-09-825-012-95 | Sequence 95, Appl |
| 59 | 62.8 | 531 | 10 | US-09-825-012-90 | Sequence 90, Appl |
| 59 | 62.8 | 729 | 10 | US-09-825-012-52 | Sequence 52, Appl |
| 59 | 62.8 | 730 | 10 | US-09-825-012-49 | Sequence 49, Appl |
| 59 | 62.8 | 731 | 10 | US-09-825-012-46 | Sequence 46, Appl |
| 59 | 62.8 | 739 | 10 | US-09-825-012-61 | Sequence 61, Appl |
| 59 | 62.8 | 740 | 10 | US-09-825-012-58 | Sequence 58, Appl |
| 59 | 62.8 | 741 | 10 | US-09-825-012-55 | Sequence 55, Appl |
| 58 | 61.7 | 20  | 10 | US-09-839-447A-9 | Sequence 9, Appl  |
| 57 | 60.6 | 17  | 9  | US-10-146-305-13 | Sequence 13, Appl |
| 57 | 60.6 | 138 | 9  | US-10-146-305-8  | Sequence 8, Appl  |
| 56 | 59.6 | 118 | 9  | US-10-141-908-2  | Sequence 2, Appl  |
| 56 | 59.6 | 118 | 9  | US-10-141-908-5  | Sequence 5, Appl  |

#### ALIGNMENTS

#### RESULT 1

US-09-943-906-70

; Sequence 70, Application US/09943906

; Patent No. US20020150571A1

; GENERAL INFORMATION:

; APPLICANT: Prusiner, Stanley B.

; Williamson, R. Anthony

; Burton, Dennis R.

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 2200 Sand Hill Road

; CITY: Menlo Park

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 94025

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/943,906

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/550,374

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Bozicevic, Karl

; REGISTRATION NUMBER: 28,807

; REFERENCE/DOCKET NUMBER: 06510/059001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-5277

; TELEFAX: 415-854-0875

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 91 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-943-906-70

Query Match      72.3%; Score 68; DB 10; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEKFKG 17
   |||||
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 2
US-09-943-906-78
; Sequence 78, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;              Williamson, R. Anthony
;              Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 78:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-943-906-78

Query Match      72.3%; Score 68; DB 10; Length 91;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEKFKG 17
   |||||
Db 24 EIWPRSGNTYYNEKFKG 40

RESULT 3
US-09-943-906-79
; Sequence 79, Application US/09943906
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;              Williamson, R. Anthony
;              Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 79:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-943-906-79

Query Match      72.3%; Score 68; DB 10; Length 92;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEKFKG 17
   |||||
Db 25 EIWPRSGNTYYNEKFKG 41

RESULT 4
US-09-943-906-85
; Sequence 85, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
;              Williamson, R. Anthony
;              Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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us-09-701-001b-2.rapb

Fri Feb 14 15:00:51 2003

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; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-09-943-906-85
72.3%; Score 68; DB 10; Length 92;
Best Local Similarity 70.6%; Pred. No. 0.0021;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYPGSGSAYNEMFKG 17
DB 25 EIWRSGNTYNEKFKG 41

RESULT 5
US-09-943-906-86
; Sequence 86, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>

```

```

;
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-943-906-86
72.3%; Score 68; DB 10; Length 95;
Best Local Similarity 70.6%; Pred. No. 0.0022;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYPGSGSAYNEMFKG 17
DB 28 EIWRSGNTYNEKFKG 44

RESULT 6
US-09-943-906-82
; Sequence 82, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-09-943-906-82
72.3%; Score 68; DB 10; Length 101;
Best Local Similarity 70.6%; Pred. No. 0.0023;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYPGSGSAYNEMFKG 17
DB 34 EIWRSGNTYNEKFKG 50

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; COUNTRY: U.S.A.
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
;
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
;
; US-09-943-906-83
;
; Query Match 72.3%; Score 68; DB 10; Length 108;
; Best Local Similarity 70.68; Pred. No. 0.0025;
; Matches 12; Conservative 2; Mismatches 3; Indels
;
; QY 1 EYPGSGSAYINEMFKG 17
; ||:| ||: |||| |||
;
; Ddb 41 EIWPGRGTYNEKFG 57
;
;
; RESULT 9
;
; US-09-943-906-68
; Sequence 68, Application US/09943906
; Patent No. US20020150571al
;
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamsson, R. Anthony
; Burton, Dennis R.
;
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
;
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807

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us-09-701-001b-2.rapb

Fri Feb 14 15:00:51 2003

REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-943-906-68

Query Match 72.3%; Score 68; DB 10; Length 114;  
Best Local Similarity 70.6%; Pred. No. 0.0026;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Db 1 EIPGSGSAYNEMFKG 17  
47 EIWPRSGNTYNEKFKG 63

RESULT 10  
US-09-943-906-76  
Sequence 76, Application US/09943906  
Patent No. US20020150571A1  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
Williamson, R. Anthony  
Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION NUMBER: US/09/943,906  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/550,374  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-943-906-76

Query Match 72.3%; Score 68; DB 10; Length 114;  
Best Local Similarity 70.6%; Pred. No. 0.0026;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 EIPGSGSAYNEMFKG 17  
Db 47 EIWPRSGNTYNEKFKG 63

RESULT 11  
US-09-943-906-77  
Sequence 77, Application US/09943906  
Patent No. US20020150571A1  
GENERAL INFORMATION:  
APPLICANT: Prusiner, Stanley B.  
Williamson, R. Anthony  
Burton, Dennis R.  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road  
CITY: Menlo Park  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION NUMBER: US/09/943,906  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/550,374  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bozicevic, Karl  
REGISTRATION NUMBER: 28,807  
REFERENCE/DOCKET NUMBER: 06510/059001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-5277  
TELEFAX: 415-854-0875  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-09-943-906-77

Query Match 72.3%; Score 68; DB 10; Length 114;  
Best Local Similarity 70.6%; Pred. No. 0.0026;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 EIPGSGSAYNEMFKG 17  
Db 47 EIWPRSGNTYNEKFKG 63

RESULT 12  
US-09-144-886-71  
Sequence 71, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize Botulinum Neurotoxins  
FILE REFERENCE: 2500.117USO

; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 71  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
; OTHER INFORMATION: IG5 region VH epitope 3  
US-09-144-886-71

Query Match 70.2%; Score 66; DB 9; Length 117;  
Best Local Similarity 75.0%; Pred. No. 0.0052;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYPGSGSAYNEMFK 16

Db 50 DIYPGSGSTNYNEFK 65

RESULT 13

; Sequence 31, Application US/08779784  
; Patent No. US20020164325A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Asakura, Kunihiko  
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,784  
; FILING DATE: 07-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,084  
; FILING DATE: 08-AUG-1996

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/236,520  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 138 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:

; ORGANISM: Mus musculus  
US-08-779-784-31

Query Match 70.2%; Score 66; DB 1; Length 138;  
Best Local Similarity 75.0%; Pred. No. 0.0061;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGSAYNEMFK 17

Db 70 IYPGSGSTYNEFK 85

RESULT 14

; Sequence 15, Application US/09861294  
; Patent No. US20020098190A1  
; GENERAL INFORMATION:  
; APPLICANT: Malaya CHATTERJEE  
; APPLICANT: Kenneth A. FOON  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: TUMORS BEARING HMEG AND CEA ANTIGENS  
; FILE REFERENCE: 304142000620  
; CURRENT APPLICATION NUMBER: US/09/861,294  
; CURRENT FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 60/049,540  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 09/096,244  
; PRIOR FILING DATE: 1998-06-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-861-294-15

Query Match 69.1%; Score 65; DB 10; Length 17;  
Best Local Similarity 62.5%; Pred. No. 0.0011;  
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYNEMFK 17

Db 2 IYPGSGSTYNEFK 17

RESULT 15

; Sequence 4, Application US/09861294  
; Patent No. US20020098190A1  
; GENERAL INFORMATION:  
; APPLICANT: Malaya CHATTERJEE  
; APPLICANT: Kenneth A. FOON  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: TUMORS BEARING HMEG AND CEA ANTIGENS  
; FILE REFERENCE: 304142000620  
; CURRENT APPLICATION NUMBER: US/09/861,294  
; CURRENT FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 60/049,540  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: 09/096,244  
; PRIOR FILING DATE: 1998-06-11  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 153  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-09-861-294-4

Query Match 69.1%; Score 65; DB 10; Length 153;

us-09-701-001b-2.rapb

Fri Feb 14 15:00:51 2003

Best Local Similarity 62.5%; Pred. No. 0.0094; 3; Mismatches 3; Indels 0; Gaps 0;

Matches 10; Conservative

QY 2 IYPGSGSAYYNEMFKG 17

1:11:1 111: 111

Db 70 IFFPGNGDTYYNQKFKG 85

Search completed: February 14, 2003, 11:21:29

Job time : 9.87097 secs



Fri Feb 14 15:00:51 2003

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 17 Seconds

(without alignments)  
96.134 Million cell updates/sec

Title: US-09-701-001b-2  
Perfect score: 94  
Sequence: 1 E1YPGSGSAYNEMFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Sched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | ID       | Description        |
|------------|-------|---------|--------------|----------|--------------------|
| 1          | 88    | 93.6    | 119          | 2 S19964 | Ig heavy chain v r |
| 2          | 88    | 93.6    | 137          | 2 PH1227 | Ig heavy chain pre |
| 3          | 82    | 87.2    | 117          | 2 S19966 | Ig heavy chain v r |
| 4          | 81    | 86.2    | 110          | 2 PH1000 | Ig heavy chain v r |
| 5          | 78    | 83.0    | 475          | 2 S01321 | Ig gamma-2b chain  |
| 6          | 76    | 80.9    | 96           | 2 PH1165 | Ig heavy chain v r |
| 7          | 73    | 77.7    | 94           | 2 G32513 | Ig heavy chain v r |
| 8          | 72    | 76.6    | 95           | 2 G37262 | Ig heavy chain v r |
| 9          | 72    | 76.6    | 111          | 2 PH0988 | Ig heavy chain v r |
| 10         | 71    | 75.5    | 119          | 2 E30562 | Ig heavy chain v r |
| 11         | 69    | 73.4    | 121          | 2 S19969 | Ig heavy chain v r |
| 12         | 67    | 71.3    | 67           | 2 H28833 | Ig kappa chain v r |
| 13         | 67    | 71.3    | 107          | 2 PH0999 | Ig heavy chain v r |
| 14         | 67    | 71.3    | 109          | 2 PH0997 | Ig heavy chain v r |
| 15         | 67    | 71.3    | 111          | 2 PH0998 | Ig heavy chain v r |
| 16         | 67    | 71.3    | 119          | 2 C30562 | Ig heavy chain v r |
| 17         | 67    | 71.3    | 119          | 2 C30562 | Ig heavy chain v r |
| 18         | 67    | 71.3    | 246          | 2 S38950 | Ig gamma chain - m |
| 19         | 67    | 71.3    | 446          | 2 S40295 | Ig gamma-2a chain  |
| 20         | 66    | 70.2    | 104          | 2 S26466 | Ig heavy chain pre |
| 21         | 66    | 70.2    | 117          | 1 HVMSA1 | Ig heavy chain pre |
| 22         | 66    | 70.2    | 137          | 2 S09956 | Ig heavy chain pre |
| 23         | 65    | 69.1    | 120          | 2 S09956 | Ig heavy chain pre |
| 24         | 65    | 69.1    | 120          | 2 PD0008 | Ig heavy chain v-D |
| 25         | 64    | 68.1    | 90           | 2 PH1159 | Ig heavy chain v r |
| 26         | 64    | 68.1    | 94           | 2 S42185 | Ig gamma chain v r |
| 27         | 64    | 68.1    | 106          | 2 PH1002 | Ig heavy chain v r |
| 28         | 64    | 68.1    | 109          | 2 PH1001 | Ig heavy chain v r |
| 29         | 64    | 68.1    | 115          | 2 A54378 | Ig heavy chain v r |

|    |    |      |     |          |                    |
|----|----|------|-----|----------|--------------------|
| 30 | 64 | 68.1 | 117 | 2 S03289 | Ig heavy chain pre |
| 31 | 62 | 66.0 | 76  | 2 B28572 | Ig heavy chain v r |
| 32 | 62 | 66.0 | 116 | 2 B28614 | Ig heavy chain v r |
| 33 | 61 | 64.9 | 115 | 2 A56700 | Ig heavy chain (an |
| 34 | 61 | 64.9 | 122 | 2 S06825 | Ig heavy chain v r |
| 35 | 61 | 64.9 | 214 | 2 PC4202 | monoclonal antibod |
| 36 | 60 | 63.8 | 93  | 2 S42182 | Ig gamma chain v r |
| 37 | 60 | 63.8 | 94  | 2 S42177 | Ig gamma chain v r |
| 38 | 60 | 63.8 | 95  | 2 S42178 | Ig gamma chain v r |
| 39 | 60 | 63.8 | 97  | 2 S42181 | Ig gamma chain v r |
| 40 | 60 | 63.8 | 101 | 2 S42179 | Ig gamma chain v r |
| 41 | 60 | 63.8 | 101 | 2 S42184 | Ig gamma chain v r |
| 42 | 60 | 63.8 | 102 | 2 S42180 | Ig gamma chain v r |
| 43 | 60 | 63.8 | 137 | 2 E29380 | Ig heavy chain pre |
| 44 | 60 | 63.8 | 469 | 2 S37483 | Ig gamma-2a chain  |
| 45 | 59 | 62.8 | 116 | 2 S26309 | Ig heavy chain v r |

ALIGNMENTS

RESULT 1

S19964

Ig heavy chain V region (M-T310) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S19964

R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19964

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <WEI>

A:Cross-references: EMBL:X65084; NID:g51964; PIDN:CAA46212.1; PID:g51965

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.6%; Score 88; DB 2; Length 119;  
Best Local Similarity 94.1%; Pred. No. 9.3e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |    |                  |    |
|----|----|------------------|----|
| QY | 1  | E1YPGSGSAYNEMFKG | 17 |
| DB | 50 | E1YPGSGSAYNEMFKG | 66 |

RESULT 2

PH1227

Ig heavy chain precursor V region (M-T310) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 23-Jul-1999

C:Accession: PH1227

R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Fliieger, D.; L

Gene 121, 271-278, 1992

A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and

A:Reference number: PH1224; MUID:93077041; PMID:1446824

A:Accession: PH1227

A:Molecule type: mRNA

A:Residues: 1-137 <WEI>

A:Cross-references: GB:S50266; NID:g260767; PIDN:AAB24321.1; PID:g260768

C:Note: this mouse sequence was hybridized and fused with a human constant region gen

C:Superfamily: immunoglobulin V region; immunoglobulin

F:1-18/Domain: signal sequence #status Predicted <SIG>

F:19-137/Product: Ig heavy chain V region #status Predicted <MAT>

F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 93.6%; Score 88; DB 2; Length 137;  
Best Local Similarity 94.1%; Pred. No. 1.1e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 |||||  
 Db 68 EIYPGSGSAYYNEMFKG 84

## RESULT 3

S19966

Ig heavy chain V region (M-T404) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 16-Aug-1996

C:Accession: S19966

R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

Submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19966

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 &lt;WEI&gt;

A:Cross-references: EMBL:X65085

Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 87.2%; Score 82; DB 2; Length 117;  
 Best Local Similarity 88.2%; Pred. No. 8.1e-06;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 |||||  
 Db 50 EIYPGSGSAYYNEMFKG 66

## RESULT 4

PH1000

Ig heavy chain V region (clone 202.105) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PH1000

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1000

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-110 &lt;TIL&gt;

A:Experimental source: B cell, strain [N2B x NZW]F1

Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 86.2%; Score 81; DB 2; Length 110;  
 Best Local Similarity 82.4%; Pred. No. 1.1e-05;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 |||||  
 Db 50 EIYPGSGSAYYNEMFKG 66

## RESULT 5

S01321

Ig gamma-2b chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999

C:Accession: S01321

R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a

A:Reference number: S01320; MUID:88329081; PMID:3138116

A:Accession: S01321

A:Molecule type: mRNA

A:Residues: 1-475 &lt;DEI&gt;

A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781

A&gt;Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-475/Product: Ig gamma-2b chain #status predicted &lt;MAT&gt;

F:159-223/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 83.0%; Score 78; DB 2; Length 475;  
 Best Local Similarity 76.5%; Pred. No. 0.00016;  
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 |||||  
 Db 69 EIYPGSGSAYYNEMFKG 85

## RESULT 6

PH1165

Ig heavy chain V region (clone 26F.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C:Accession: PH1165

R:Schitteck, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1165

A:Molecule type: DNA

A:Residues: 1-96 &lt;SCH&gt;

A:Experimental source: B cell

Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-96/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.9%; Score 76; DB 2; Length 96;  
 Best Local Similarity 81.2%; Pred. No. 5.9e-05;  
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17  
 |||||  
 Db 51 IYPGSGNTYNEKFKG 66

## RESULT 7

G32513

Ig heavy chain V region (BXW14) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Aug-1996

C:Accession: G32513

R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Duchosal, M.A.

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization a

A:Reference number: A94689; MUID:88331394; PMID:3138286

A:Accession: G32513

A:Molecule type: DNA

A:Residues: 1-94 &lt;KOF&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 77.7%; Score 73; DB 2; Length 94;  
 Best Local Similarity 76.5%; Pred. No. 0.00017;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 |||||  
 Db 25 EIYPRSGNTYNEKFKG 41

## RESULT 8

G37262

Ig heavy chain V region (14D2) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 16-Aug-1996  
 C:Accession: G37262  
 R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.  
 J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same antigen  
 A:Reference number: A38601; MUID:91115823; PMID:1703527  
 A:Accession: G37262  
 A:Molecule type: mRNA  
 A:Status: preliminary; not compared with conceptual translation  
 A:Residues: 1-95 <GOS>  
 A:Cross-references: GB:M57993  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-84/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 72; DB 2; Length 95;  
 Best Local Similarity 76.5%; Pred. No. 0.00025;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 Db 36 ETLPGSGSSYNEKFKG 52  
 ||||| ||||| |||||

RESULT 9  
 PH0988  
 Ig heavy chain V region (clone 17s-c3) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0988  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells  
 A:Reference number: PH0971; MUID:92381444; PMID:1512540  
 A:Accession: PH0988  
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
 A:Residues: 1-111 <TIL>  
 A:Experimental source: B cell, strain [NZB x NZW]F1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 72; DB 2; Length 111;  
 Best Local Similarity 76.5%; Pred. No. 0.0003;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 Db 50 EIYPRSGNIYNEKFKG 66  
 ||||| ||||| |||||

RESULT 10  
 E30562  
 Ig heavy chain V region (27.10.2) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 16-Aug-1996  
 C:Accession: E30562  
 R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.  
 J. Immunol. 142, 888-893, 1989  
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site  
 A:Reference number: A30562; MUID:89110066; PMID:2464031  
 A:Accession: E30562  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <SIK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 71; DB 2; Length 119;

Best Local Similarity 76.5%; Pred. No. 0.00046;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFKG 17  
 Db 50 EIPPGSGSTKYNEKFKG 66  
 ||||| ||||| |||||

RESULT 11  
 S19969  
 Ig heavy chain V region (M-T413) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S19969  
 R:Weissenhorn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.  
 submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963  
 A:Accession: S19969  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-121 <WEI>  
 A:Cross-references: EMBL:X65086; NID:951974; PIDN:CAA46214.1; PID:951975  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 69; DB 2; Length 121;  
 Best Local Similarity 81.2%; Pred. No. 0.00098;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIYPGSGSAYYNEMFK 16  
 Db 50 EIYPGSGSNTYNEKFK 65  
 ||||| ||||| |||||

RESULT 12  
 H28833  
 Ig kappa chain V region (HP22.202.16) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-May-1997  
 C:Accession: H28833  
 R:Corbet, S.; Hirn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.  
 J. Immunol. 141, 779-784, 1988  
 A:Title: Allelic manipulation of the CAT idiotype cascade. Immunization of C57BL/6 mice with a monoclonal anti-idiotypic cascade  
 A:Reference number: A92827; MUID:88285674; PMID:3135311  
 A:Accession: H28833  
 A:Molecule type: mRNA

A:Residues: 1-67 <COR>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 71.3%; Score 67; DB 2; Length 67;  
 Best Local Similarity 75.0%; Pred. No. 0.0011;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17  
 Db 20 IYPGSGNTKYNEKFKG 35  
 ||||| ||||| |||||

RESULT 13  
 PH0999  
 Ig heavy chain V region (clone 74-cl) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0999  
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
 J. Exp. Med. 176, 761-779, 1992  
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells  
 A:Reference number: PH0971; MUID:92381444; PMID:1512540  
 A:Accession: PH0999  
 A:Status: nucleic acid sequence not shown

Job time : 17 secs

A:Molecule type: mRNA  
A:Residues: 1-107 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 67; DB 2; Length 107;  
Best Local Similarity 75.0%; Pred. No. 0.0018;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFMFG 17  
|||||: ||| |||  
Db 50 IYPGSGNTRYNEKFG 65

# RESULT 14

PH0997  
Ig heavy chain V region (clone 17s-c2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
Accession: PH0997  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH0997  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-109 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 67; DB 2; Length 109;  
Best Local Similarity 75.0%; Pred. No. 0.0018;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFMFG 17  
|||||: ||| |||  
Db 51 IYPGSGNTRYNEKFG 66

# RESULT 15

PH0998  
Ig heavy chain V region (clone 165.3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
Accession: PH0998  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH0998  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-111 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 67; DB 2; Length 111;  
Best Local Similarity 75.0%; Pred. No. 0.0018;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFMFG 17  
|||||: ||| |||  
Db 51 IYPGSGNTRYNEKFG 66

Search completed: February 14, 2003, 11:19:44



Fri Feb 14 15:00:51 2003

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OM protein - protein search, using sw model  
Run on: February 14, 2003, 11:05:27 ; Search time 8.77419 Seconds  
(without alignments)  
80.360 Million cell updates/sec

Title: US-09-701-001B-2  
Perfect score: 94  
Sequence: 1 EIYPGSGSAYINEMFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues 112892  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 66    | 70.2        | 117    | 1 HV52_MOUSE | P06327 mus musculus |
| 2          | 52    | 55.3        | 120    | 1 HV03_MOUSE | P01747 mus musculus |
| 3          | 52    | 55.3        | 121    | 1 HV01_MOUSE | P01746 mus musculus |
| 4          | 51    | 54.3        | 140    | 1 HV02_MOUSE | P01748 mus musculus |
| 5          | 48    | 51.1        | 117    | 1 HV04_MOUSE | P45492 campylobact  |
| 6          | 48    | 51.1        | 372    | 1 Y983_CAME  | P01756 mus musculus |
| 7          | 47    | 50.0        | 117    | 1 HV12_MOUSE | P01757 mus musculus |
| 8          | 47    | 50.0        | 117    | 1 HV13_MOUSE | P06330 mus musculus |
| 9          | 47    | 50.0        | 118    | 1 HV51_MOUSE | Q06067 escherichia  |
| 10         | 46    | 48.9        | 608    | 1 ATOS_ECOLI | P03980 mus musculus |
| 11         | 46    | 48.9        | 138    | 1 HV48_MOUSE | P01749 mus musculus |
| 12         | 45    | 47.9        | 117    | 1 HV05_MOUSE | P33292 pichia past  |
| 13         | 45    | 47.9        | 576    | 1 PEX5_PICPA | P36334 human coron  |
| 14         | 45    | 47.9        | 1353   | 1 VGL2_CVHOC | P25190 bovine coro  |
| 15         | 45    | 47.9        | 1363   | 1 VGL2_CVBF  | P25191 bovine coro  |
| 16         | 45    | 47.9        | 1363   | 1 VGL2_CVBL9 | P25192 bovine coro  |
| 17         | 45    | 47.9        | 1363   | 1 VGL2_CVBL  | P15777 bovine coro  |
| 18         | 45    | 47.9        | 1363   | 1 VGL2_CVBL  | P25193 bovine coro  |
| 19         | 45    | 47.9        | 1363   | 1 VGL2_CVBO  | P25194 bovine coro  |
| 20         | 45    | 47.9        | 1363   | 1 VGL2_CVBO  | P01753 mus musculus |
| 21         | 44    | 46.8        | 117    | 1 HV09_MOUSE | P01754 mus musculus |
| 22         | 44    | 46.8        | 117    | 1 HV10_MOUSE | P01758 mus musculus |
| 23         | 44    | 46.8        | 117    | 1 HV14_MOUSE | P06328 mus musculus |
| 24         | 44    | 46.8        | 117    | 1 HV47_MOUSE | P01751 mus musculus |
| 25         | 44    | 46.8        | 139    | 1 HV07_MOUSE | P36261 gallus gall  |
| 26         | 44    | 46.8        | 405    | 1 SDC3_CHICK | P35718 saccharomyc  |
| 27         | 43    | 45.7        | 212    | 1 RPY1_YEAST | P01750 mus musculus |
| 28         | 42    | 44.7        | 117    | 1 HV06_MOUSE | P06329 mus musculus |
| 29         | 42    | 44.7        | 120    | 1 HV50_MOUSE | Q64519 mus musculus |
| 30         | 42    | 44.7        | 442    | 1 SDC3_MOUSE | P33671 rattus norv  |
| 31         | 42    | 44.7        | 442    | 1 SDC3_RAT   | P79430 sus scrofa   |
| 32         | 42    | 44.7        | 503    | 1 CPV2_PIG   | Q02934 clostridium  |
| 33         | 42    | 44.7        | 879    | 1 GUN1_CLOTH |                     |

34 42 44.7 986 1 GUNZ\_CLOSR  
35 41 43.6 163 1 SFAS\_ECOLI  
36 41 43.6 469 1 YXIA\_BACSU  
37 41 43.6 683 1 AMOH\_ARTGO  
38 41 43.6 695 1 MDLI\_YEAST  
39 41 43.6 976 1 KIT\_HUMAN  
40 40 42.6 101 1 RM06\_MARPO  
41 40 42.6 117 1 HV55\_MOUSE  
42 40 42.6 137 1 HV11\_MOUSE  
43 40 42.6 257 1 DLHH\_SULSO  
44 40 42.6 489 1 OCLN\_POTIR  
45 40 42.6 502 1 SPEL\_LYCES

P23659 clostridium  
P13430 escherichia  
P42293 bacillus su  
Q59118 arthrobacte  
P33310 saccharomyc  
P10721 homo sapien  
P26861 marchantia  
P18526 mus musculu  
P01755 mus musculu  
P95862 sulfolobus  
Q28793 potorous tr  
P49726 lycopersico

ALIGNMENTS

RESULT 1  
HV52\_MOUSE  
ID HV52\_MOUSE STANDARD; PRT; 117 AA.  
AC P06327:  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region VH558 Al/A4 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85099340; PubMed=2578321;  
RA Yancopoulos G.D., Alt F.W.;  
RT "Developmentally controlled and tissue-specific expression of  
unrearranged VH gene segments.";  
RL Cell 40:271-281(1985).  
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CC EMBL; M13787; AAA38499.1;  
DR PIR; A02029; HVMSA1.  
DR HSSP; P01810; 2PBJ.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117  
FT DOMAIN 20 49  
FT DOMAIN 50 54  
FT DOMAIN 55 68  
FT DOMAIN 69 85  
FT DOMAIN 86 117  
FT DISULFID 41 115  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;  
IG HEAVY CHAIN V REGION VH558 Al/A4.  
FRAMEWORK-1.  
COMPLEMENTARITY-DETERMINING-1.  
FRAMEWORK-2.  
COMPLEMENTARITY-DETERMINING-2.  
FRAMEWORK-3.  
BY SIMILARITY.

Query Match 70.2%; Score 66; DB 1; Length 117;  
Best Local Similarity 75.0%; Pred. No. 0.0006; 0; Mismatches 4; Indels 0; Gaps 0;  
Matches 12; Conservative 0;

Qy 2 IYPGSGSAYINEMFKG 17

Db 70 IYPGSGSKYNEKFKG 85

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RESULT 2
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR: A02028; HVMSG7.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 55.3%; Score 52; DB 1; Length 120;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFKG 17
| ||:| ||| |||
Db 50 INPGNGYTKYNEFKG 65

RESULT 3
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3391-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RA Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR: A02027; GYMS11.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF000047; Ig; 1.

us-09-701-001b-2.rsp
```

```
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 55.3%; Score 52; DB 1; Length 121;
Best Local Similarity 52.9%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EYPGSGSAYYNEFKG 17
:||||| | ||:|
Db 50 DIYPGGGFTYNDNLKG 66

RESULT 4
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
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CC -----
DR EMBL; J00493; AAA38128.1; -.
DR PIR; A02028; HVMSG7.
DR HSP: P01810; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF000047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 54.3%; Score 51; DB 1; Length 140;
Best Local Similarity 62.5%; Pred. No. 0.21;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEFKG 17
| ||:| ||| |||
Db 70 INPGNGYTKYNEFKG 85

RESULT 5
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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DE Iq heavy chain V region 23 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.; variable region contribution to the NpB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.;  
 RL Cell 24:625-637(1981).  
 CC -!- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
 DR PIR: A02030; HVMS23.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; Igv; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;  
 Query Match 51.1%; Score 48; DB 1; Length 117;  
 Best Local Similarity 60.0%; Pred. No. 0.54;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 IYPGSGSAYNEMFK 16  
 DB 70 INPGNGGTNYNEKFK 84  
 RESULT 6  
 Y983\_CAMJE  
 ID P45492; Q9PNV6;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical lipoprotein Cj0983 precursor.  
 GN Cj0983.  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
 OC Campylobacter.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43431 / TGH 9011;  
 RX MEDLINE=95247673; PubMed=7730270;  
 RA Hani E.K., Chan V.L.;  
 RA "Expression and characterization of Campylobacter jejuni  
 RT benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia  
 RT coli".  
 RL J. Bacteriol. 177:2396-2402(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 11168;  
 RX MEDLINE=20150912; PubMed=10688204;  
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churche C.,  
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,  
 RA Jagsels K., Karyshev A.V., Moule S., Pallen M.J., Penn C.W.,  
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

RA Whitehead S., Barrell B.G.;  
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
 RT reveals hypervariable sequences.";  
 RL Nature 403:665-668(2000).  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 CC (Potential).  
 CC [1]  
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 CC [1]  
 DR EMBL: Z36940; CAA85399.1; --  
 DR EMBL: ALI39076; CAB73239.1; --  
 KW Hypothetical protein; Membrane; Lipoprotein; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 372 HYPOTHETICAL LIPOPROTEIN Cj0983.  
 FT LIPID 18 18 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT CONFLICT 78 78 T -> A (IN REF. 1).  
 FT CONFLICT 83 83 D -> N (IN REF. 1).  
 FT CONFLICT 105 105 K -> E (IN REF. 1).  
 FT CONFLICT 157 157 S -> R (IN REF. 1).  
 FT CONFLICT 227 227 V -> A (IN REF. 1).  
 FT CONFLICT 230 230 K -> E (IN REF. 1).  
 FT CONFLICT 278 278 A -> T (IN REF. 1).  
 FT CONFLICT 289 289 A -> T (IN REF. 1).  
 FT CONFLICT 353 353 A -> V (IN REF. 1).  
 FT CONFLICT 370 371 AS -> SYFK (IN REF. 1).  
 SQ SEQUENCE 372 AA; 42164 MW; 3C562051EBC638B4 CRC64;  
 Query Match 51.1%; Score 48; DB 1; Length 372;  
 Best Local Similarity 45.5%; Pred. No. 1.9;  
 Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 1;  
 QY 1 EYPGSGSA-----YYNEMFK 16  
 DB 100 EYKGNKASISIKYNDLFK 121  
 RESULT 7  
 HV12\_MOUSE  
 ID HV12\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01756;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ig heavy chain V region MOPC 104E.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.  
 RX MEDLINE=83075344; PubMed=6816276;  
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
 RA Hood L.E.;  
 RT "Complete amino acid sequence of a mouse mu chain: homology among  
 RT heavy chain constant region domains";  
 RL Biochemistry 21:5415-5424(1982).  
 CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA  
 CC PROTEIN HAS ALSO BEEN DETERMINED.  
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
 DR PIR: A02039; MHMS4E.  
 DR HSSP: P01789; IMCP.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; Igv; 1.  
 DR Immunoglobulin V region; Glycoprotein.  
 KW

```

RT  "A V region determinant (idiotope) expressed at high frequency in B
RL  lymphocytes is encoded by a large set of antibody structural genes." ;
DR  PIR: A02040; MHMS38.
DR  HSSP: P01789; LMCP.
DR  InterPro: IPR003006; Iq_MHC.
DR  InterPro: IPR003596; Iq_V.
DR  Pfam: PF00047; Iq_1.
DR  SMART: SM00406; IGV; 1.
DR  Immunoglobulin V region.
FT  DOMAIN 1 98 V SEGMENT.
FT  DOMAIN 99 104 D SEGMENT.
FT  DOMAIN 105 118 J SEGMENT.
FT  DISULFID 22 96 BY SIMILARITY.
FT  NON_TER 118 118
SQ  SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 50.0%; Score 47; DB 1; Length 118;
Best Local Similarity 47.1%; Pred. No. 0.7;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELYPGSGSAYYNEMFKG 17
Db 50 DPNPNGGTSYNQKFKG 66
::: ||: ||: ||:

RESULT 10
ATOS_ECOLI STANDARD; PRT; 608 AA.
ID ATOS_ECOLI
AC Q06067;
DT 01-FEB-1995 (Rel. 31, Created)
DD 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sensor protein atos (EC 2.7.3.-).
GN ATOS OR B2219.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=K12;
RX MEDLINE=93348226; PubMed=8346225;
RA Canellakis E.S., Paterakis A.A., Huang S.-C., Panagiotidis C.A.,
RA Kyriakidis D.S.;
RT "Identification, cloning, and nucleotide sequencing of the ornithine
RT decarboxylase antizyme gene of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7129-7133(1993).
RN [2]
RP SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden C.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12." ;
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map." ;
RL DNA Res. 3:379-392(1996).
CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM ATOS/ATOC;
CC MAY ACTIVATE ATOC BY PHOSPHORYLATION.
CC

```

CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC CC (Potential).  
 CC CC -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.  
 CC CC -!- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.  
 CC CC -!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.  
 CC CC -----  
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 CC CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC CC -----  
 CC CC EMBL; L13078; AAA23449.1; -;  
 CC CC EMBL; AE000311; AAC75279.1; -;  
 CC CC EMBL; D50851; BAAL6015.1; -;  
 CC CC EcoGene; E311667; atos.  
 CC CC InterPro; IPR003594; ATPbind\_ATPase.  
 CC CC InterPro; IPR004358; Bact\_sens\_pr\_C.  
 CC CC InterPro; IPR003660; HAMP.  
 CC CC InterPro; IPR004359; HIS\_KIN\_sig.  
 CC CC InterPro; IPR003661; His\_KINa.  
 CC CC InterPro; IPR000700; PAS-assoc\_C.  
 CC CC InterPro; IPR000014; PAS\_domain.  
 CC CC Pfam; PF00512; signal; 1.  
 CC CC Pfam; PF00672; HAMP; 1.  
 CC CC Pfam; PF00989; PAS; 1.  
 CC CC Pfam; PF02518; HATPase\_c; 1.  
 CC CC PRINTS; PR00344; BCTRLSENSOR.  
 CC CC SMART; SM00304; HAMP; 1.  
 CC CC SMART; SM00387; HATPase\_c; 1.  
 CC CC SMART; SM00388; Hiska; 1.  
 CC CC SMART; SM00091; PAS; 1.  
 CC CC TIGRFAMs; TIGR00229; sensory\_box; 1.  
 CC CC PROSITE; PS50109; HIS\_KIN; 1.  
 CC CC PROSITE; PS50113; PAC; 1.  
 CC CC PROSITE; PS50112; PAS; 1.  
 CC CC Sensory transduction; Transferase; Kinase; Phosphorylation;  
 CC CC Transmembrane; Inner membrane; Complete proteome.  
 CC CC TRANSMEM 16 36 POTENTIAL.  
 CC CC TRANSMEM 190 210 POTENTIAL.  
 CC CC DOMAIN 326 325 PAS.  
 CC CC DOMAIN 326 382 PAC.  
 CC CC DOMAIN 395 602 HISTIDINE KINASE.  
 CC CC MOD\_RES 398 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 CC CC TRANSMEM 584 604 POTENTIAL.  
 CC CC SEQUENCE 608 AA; 67789 MW; 4669888F98985C9C CRC64;  
 CC CC -----  
 CC CC Query Match 50.0%; Score 47; DB 1; Length 608;  
 CC CC Best Local Similarity 58.3%; Pred. No. 4.8;  
 CC CC Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 CC CC -----  
 CC CC Y 3 YPGSGSAYNEM 14  
 CC CC :||| : ||| :||| :  
 CC CC Db 96 FPGICAGYNNKM 107  
 CC CC -----  
 CC CC RESULT 11  
 CC CC ID HV48\_MOUSE STANDARD; PRT; 138 AA.  
 CC CC AC P03980;  
 CC CC DT 23-OCT-1986 (Rel. 02, Created)  
 CC CC DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 CC CC DT 15-JUL-1999 (Rel. 36, Last annotation update)  
 CC CC DE Ig heavy chain V region TEPC 1017 precursor.  
 CC CC OS Mus musculus (Mouse).  
 CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC CC OX NCBI\_TaxID=10090;  
 CC CC RN [1]  
 CC CC RP SEQUENCE FROM N.A.  
 CC CC RX MEDLINE=84248078; PubMed=6429663;  
 CC CC -----

RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,  
 RA Tucker P.W.;  
 RA "Illegitimate recombination generates a class switch from C mu to C  
 RT delta in an IgD-secreting plasmacytoma.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).  
 DR PIR; A02033; HVMST7.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.  
 FT DOMAIN 21 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 128 138 FRAMEWORK-4.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 138 138  
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;  
 CC CC -----  
 CC CC Query Match 48.9%; Score 46; DB 1; Length 138;  
 CC CC Best Local Similarity 56.2%; Pred. No. 1.4;  
 CC CC Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 CC CC -----  
 CC CC QY 1 EIVPGSGSAYNEMFK 16  
 CC CC :||| : ||| :||| :  
 CC CC Db 69 EINPDGRSNYNEFK 84  
 CC CC -----  
 CC CC RESULT 12  
 CC CC ID HV05\_MOUSE STANDARD; PRT; 117 AA.  
 CC CC AC P01749;  
 CC CC DT 21-JUL-1986 (Rel. 01, Created)  
 CC CC DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 CC CC DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 CC CC DE Ig heavy chain V region 3 precursor.  
 CC CC OS Mus musculus (Mouse).  
 CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC CC OX NCBI\_TaxID=10090;  
 CC CC RN [1]  
 CC CC RP SEQUENCE FROM N.A.  
 CC CC RC STRAIN=C57BL/6;  
 CC CC RX MEDLINE=81234548; PubMed=6788376;  
 CC CC RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 CC CC RA Baltimore D.;  
 CC CC RT "Heavy chain variable region contribution to the NPb family of  
 CC CC antibodies: somatic mutation evident in a gamma 2a variable region.";  
 CC CC Cell 24:625-637(1981).  
 CC CC -!- MISCELLANEOUS: THIS GENE LINE GENE BELONGS TO A SET OF CLOSELY  
 CC CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
 CC CC -----  
 CC CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 CC CC -----  
 CC CC EMBL; J00536; AAA38605.1; -;  
 CC CC PIR; A02031; HVM33.  
 CC CC HSSP; P01810; 2FBJ.  
 CC CC InterPro; IPR003006; Ig\_MHC.  
 CC CC InterPro; IPR003596; Ig\_V.  
 CC CC Pfam; PF00047; Ig; 1.  
 CC CC SMART; SM00406; IGV; 1.  
 CC CC SEQUENCE FROM N.A.  
 CC CC RX MEDLINE=84248078; PubMed=6429663;  
 CC CC -----



|                       |                       |               |                                   |          |  |
|-----------------------|-----------------------|---------------|-----------------------------------|----------|--|
| CHAIN                 | 758                   | 1353          | SPIKE PROTEIN S2.                 |          |  |
| DOMAIN                | 18                    | 1298          | EXTRACELLULAR (POTENTIAL).        |          |  |
| TRANSMEM              | 1299                  | 1318          | POTENTIAL.                        |          |  |
| DOMAIN                | 1319                  | 1353          | CYTOPLASMIC (POTENTIAL).          |          |  |
| DOMAIN                | 1319                  | 1336          | CYS-RICH.                         |          |  |
| CARBOHYD              | 59                    | 59            | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 133                   | 133           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 146                   | 146           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 202                   | 202           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 363                   | 363           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 441                   | 441           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 496                   | 496           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 639                   | 639           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 666                   | 666           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 686                   | 686           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 704                   | 704           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 729                   | 729           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 778                   | 778           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 927                   | 927           | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 1184                  | 1184          | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 1214                  | 1214          | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 1224                  | 1224          | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 1243                  | 1243          | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 1257                  | 1257          | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| CARBOHYD              | 1278                  | 1278          | N-LINKED (GLCNAC. .) (POTENTIAL). |          |  |
| SEQUENCE              | 1353 AA;              | 150088 MW;    | 7B1CE3CDBD1A902A CRC64;           |          |  |
| Query Match           | 47.9%;                | Score 45;     | Length 1353;                      |          |  |
| Best Local Similarity | 60.0%;                | Pred. No. 24; |                                   |          |  |
| Matches               | 9; Conservative       | 0; Mismatches | 6; Indels                         | 0; Gaps  |  |
| QY                    | 3 YPGSGSAYNEMFKG 17   |               |                                   |          |  |
|                       |                       |               |                                   |          |  |
| DD                    | 68 YPTSGSTYENMALKG 82 |               |                                   |          |  |
| RESULT 15             |                       |               |                                   |          |  |
| VGL2_CVBF             |                       |               |                                   |          |  |
| ID                    | VGL2_CVBF             | STANDARD;     | PRT;                              | 1363 AA. |  |

Search completed: February 14, 2003, 11:16:20  
Job time : 9.77419 secs

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RESULT 15
VGL2_CVBF
ID VGL2_CVBF STANDARD; PRT: 1363 AA.
AC P25190;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein)
DE [Contains: Spike protein S1 (90B); Spike protein S2 (90A)].
GN S.
BO Bovine coronavirus (strain F15).
VR Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
NC NCBI_TaxID=11129;
[1]
SEQUENCE FROM N.A.
MEDLINE=90171938; PubMed=2155300;
RA Boireau P., Cruciere C., Laporte J.;
RX "Nucleotide sequence of the glycoprotein S gene of bovine enteric
RT coronavirus and comparison with the S proteins of two mouse hepatitis
RT virus strains.";
RL J. Gen. Virol. 71:487-492(1990).
CC -!- FUNCTION: THE PEPLIMER PROTEIN MEDIATES THE BINDING OF VIRIONS
CC TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00731; BAA0631.1; -
DR PIR; A34151; VGIHF1.
DR InterPro; IPR002552; Corona_S2.
DR Pfam; PF01601; Corona_S2; 1.
DR

```





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 35,371 Seconds  
(without alignments)  
99.030 Million cell updates/sec

Title: US-09-701-001b-2  
Perfect score: 94  
Sequence: 1 E1YPCGSAAYNEMFKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Search: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*

- 1: sp.archaea.\*
- 2: sp.bacteria.\*
- 3: sp.fungi.\*
- 4: sp.human.\*
- 5: sp.invertebrate.\*
- 6: sp.mammal.\*
- 7: sp.mhc.\*
- 8: sp.organelle.\*
- 9: sp.phage.\*
- 10: sp.plant.\*
- 11: sp.rodent.\*
- 12: sp.virus.\*
- 13: sp.vertebrate.\*
- 14: sp.unclassified.\*
- 15: sp.virus.\*
- 16: sp.bacteriaph.\*
- 17: sp.archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | ID        | Description         |
|------------|-------|-------|--------|-----------|---------------------|
| 1          | 76    | 80.9  | 463    | 11 Q99LC4 | Q99LC4 mus musculus |
| 2          | 70    | 74.5  | 473    | 11 Q99LC4 | Q99LC4 mus musculus |
| 3          | 68    | 72.3  | 110    | 11 Q99LC4 | Q99LC4 mus musculus |
| 4          | 67    | 71.3  | 613    | 11 Q99LC4 | Q99LC4 mus musculus |
| 5          | 66    | 70.2  | 143    | 11 Q99LC4 | Q99LC4 mus musculus |
| 6          | 63    | 67.0  | 481    | 11 Q99LC4 | Q99LC4 mus musculus |
| 7          | 62    | 66.0  | 147    | 11 Q99LC4 | Q99LC4 mus musculus |
| 8          | 62    | 66.0  | 168    | 11 Q99LC4 | Q99LC4 mus musculus |
| 9          | 59    | 62.8  | 110    | 11 Q99LC4 | Q99LC4 mus musculus |
| 10         | 58    | 61.7  | 473    | 11 Q99LC4 | Q99LC4 mus musculus |
| 11         | 55    | 58.5  | 111    | 11 Q99LC4 | Q99LC4 mus musculus |
| 12         | 50    | 53.2  | 118    | 11 Q99LC4 | Q99LC4 mus musculus |
| 13         | 50    | 53.2  | 335    | 16 Q99LC4 | Q99LC4 mus musculus |
| 14         | 48    | 51.1  | 121    | 16 Q99LC4 | Q99LC4 mus musculus |
| 15         | 48    | 51.1  | 372    | 2 Q99LC4  | Q99LC4 mus musculus |
| 16         | 48    | 51.1  | 489    | 11 Q99LC4 | Q99LC4 mus musculus |

|    |    |      |      |           |                     |
|----|----|------|------|-----------|---------------------|
| 17 | 47 | 50.0 | 117  | 11 Q99LC4 | Q99LC4 mus musculus |
| 18 | 47 | 50.0 | 117  | 11 Q99LC4 | Q99LC4 mus musculus |
| 19 | 47 | 50.0 | 187  | 8 Q99LC4  | Q99LC4 mus musculus |
| 20 | 47 | 50.0 | 373  | 9 Q99LC4  | Q99LC4 mus musculus |
| 21 | 47 | 50.0 | 373  | 16 Q99LC4 | Q99LC4 mus musculus |
| 22 | 46 | 48.9 | 474  | 11 Q99LC4 | Q99LC4 mus musculus |
| 23 | 45 | 47.9 | 278  | 11 Q99LC4 | Q99LC4 mus musculus |
| 24 | 45 | 47.9 | 373  | 9 Q99LC4  | Q99LC4 mus musculus |
| 25 | 45 | 47.9 | 373  | 9 Q99LC4  | Q99LC4 mus musculus |
| 26 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 27 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 28 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 29 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 30 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 31 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 32 | 45 | 47.9 | 768  | 12 Q99LC4 | Q99LC4 mus musculus |
| 33 | 45 | 47.9 | 791  | 12 Q99LC4 | Q99LC4 mus musculus |
| 34 | 45 | 47.9 | 1361 | 12 Q99LC4 | Q99LC4 mus musculus |
| 35 | 45 | 47.9 | 1361 | 12 Q99LC4 | Q99LC4 mus musculus |
| 36 | 45 | 47.9 | 1363 | 12 Q99LC4 | Q99LC4 mus musculus |
| 37 | 45 | 47.9 | 1363 | 12 Q99LC4 | Q99LC4 mus musculus |
| 38 | 45 | 47.9 | 1363 | 12 Q99LC4 | Q99LC4 mus musculus |
| 39 | 45 | 47.9 | 1363 | 12 Q99LC4 | Q99LC4 mus musculus |
| 40 | 45 | 47.9 | 1363 | 12 Q99LC4 | Q99LC4 mus musculus |
| 41 | 45 | 47.9 | 1363 | 12 Q99LC4 | Q99LC4 mus musculus |
| 42 | 44 | 46.8 | 137  | 11 Q99LC4 | Q99LC4 mus musculus |
| 43 | 44 | 46.8 | 139  | 11 Q99LC4 | Q99LC4 mus musculus |
| 44 | 44 | 46.8 | 140  | 11 Q99LC4 | Q99LC4 mus musculus |
| 45 | 44 | 46.8 | 141  | 11 Q99LC4 | Q99LC4 mus musculus |

## ALIGNMENTS

## RESULT 1

|        |  |        |              |      |         |
|--------|--|--------|--------------|------|---------|
| Q99LC4 | ID   | Q99LC4 | PRELIMINARY; | PRT; | 463 AA. |
| AC     | Q99LC4;  |        |              |      |         |
| DT     | 01-JUN-2001 (TrEMBLrel. 17, Created)                               |        |              |      |         |
| DT     | 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)                  |        |              |      |         |
| DT     | 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)                |        |              |      |         |
| DE     | Similar to RIKEN cDNA 1810060009 gene.                             |        |              |      |         |
| GN     | IGH-4.   |        |              |      |         |
| OS     | Mus musculus (Mouse).  |        |              |      |         |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |        |              |      |         |
| OC     | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |        |              |      |         |
| OX     | NCBI_TaxID=10090;  |        |              |      |         |
| RN     | [1]  |        |              |      |         |
| RP     | SEQUENCE FROM N.A.   |        |              |      |         |
| RA     | Strausberg R.;   |        |              |      |         |
| RL     | Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.            |        |              |      |         |
| DR     | EMBL; BC03435; AA03435.1; -  |        |              |      |         |
| DR     | HSP; P01842; 7FAB.   |        |              |      |         |
| DR     | MGI; MGI:96446; Igh-4.   |        |              |      |         |
| DR     | InterPro; IPR003599; Ig.   |        |              |      |         |
| DR     | InterPro; IPR003597; Ig.cl.  |        |              |      |         |
| DR     | InterPro; IPR003600; Ig.MHC.                                       |        |              |      |         |
| DR     | InterPro; IPR003006; Ig.MHC.                                       |        |              |      |         |
| DR     | InterPro; IPR003596; Ig.v.   |        |              |      |         |
| DR     | Pfam; PF00047; Ig. 4.  |        |              |      |         |
| DR     | SMART; SM00409; IG; 2.   |        |              |      |         |
| DR     | SMART; SM00407; IGcl; 2.   |        |              |      |         |
| DR     | SMART; SM00406; IGV; 1.  |        |              |      |         |
| DR     | SMART; SM00410; IG.Like; 1.  |        |              |      |         |
| DR     | PROSITE; PS00290; IG.MHC; UNKNOWN_1.                               |        |              |      |         |
| SQ     | SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;                 |        |              |      |         |

Query Match 80.9%; Score 76; DB 11; Length 463;  
Best Local Similarity 76.5%; Pred. No. 0.00047;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 E1YPCGSAAYNEMFKG 17  
|||||||:|:|:|

Db 69 E1YPGSGNTYYSEKFG 85

## RESULT 2

Q9D8L4

ID Q9D8L4 PRELIMINARY; PRT; 473 AA.  
 AC Q9D8L4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 181006009Rik protein.  
 GN IGH-1 OR 181006009RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Rono H., Baldarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 DR EMBL; AK007918; BAB25349.1; -.  
 DR HSSP; P01842; 7FAB.  
 DR MGD; MGI:96443; Igh-1.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003600; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; Igc1; 3.  
 DR SMART; SM00406; Igv; 1.  
 DR SMART; SM00410; Ig-like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 473 AA; 51699 MW; 9DE57A514475FEB CRC64;

Query Match 74.5%; Score 70; DB 11; Length 473;

Best Local Similarity 76.5%; Pred. No. 0.0045;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 E1YPGSGNTYYSEKFG 17

Db 69 K1GPGSGTYYNEKFG 85

## RESULT 3

Q9JL83

ID Q9JL83 PRELIMINARY; PRT; 110 AA.  
 AC Q9JL83;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Anti-myosin immunoglobulin heavy chain variable region

DE (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RX MEDLINE=20448942; PubMed=10992488;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-Cell-dependent antibody response to the dominant epitope of

RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive

RL Infect. Immun. 68:5803-5808 (2000).

DR EMBL; AF206023; AAF69321.1; -.

DR HSSP; P01810; 2FBJ.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; Igv; 1.

FT NON\_TER 1

FT NON\_TER 110 110

SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 72.3%; Score 68; DB 11; Length 110;

Best Local Similarity 75.0%; Pred. No. 0.0019;

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEKFG 17

Db 43 IYPGDGDYNGKFG 58

## RESULT 4

Q8VCX7

ID Q8VCX7 PRELIMINARY; PRT; 613 AA.  
 AC Q8VCX7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 67.9 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Salivary Gland;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018315; AAH18315.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 5.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; Igc1; 4.  
 DR SMART; SM00406; Igv; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 71.3%; Score 67; DB 11; Length 613;

Best Local Similarity 76.5%; Pred. No. 0.019;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYYNEKFG 17

Db 69 E1LPGSGSTYNEKFG 85

## RESULT 5

Q92400  
ID Q92400 PRELIMINARY; PRT; 143 AA.  
AC Q92400;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE V165-D-J-C mu protein (Fragment).  
GN V165-D-J-C MU.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CS7BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB069915; BAB63931.1; -;  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
FT NON\_TER 1  
FT 143  
SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;  
Query Match 70.2%; Score 66; DB 11; Length 143;  
Best Local Similarity 75.0%; Pred. No. 0.0054;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 EYPGSGSAYYNEFK 16  
Db :||||| ||| ||  
50 DIYPGSGSTNYNEKFG 65  
RESULT 6  
Q91WT1 PRELIMINARY; PRT; 481 AA.  
ID Q91WT1  
AC Q91WT1;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical 52.1 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013490; AAH13490.1; -;  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;  
Query Match 67.0%; Score 63; DB 11; Length 481;  
Best Local Similarity 68.8%; Pred. No. 0.063;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 2 IYPGSGSAYYNEFK 17  
Db :||||| ||| |||  
70 IYPGDGNKYNKFKG 85  
RESULT 7  
Q925S3 PRELIMINARY; PRT; 147 AA.  
ID Q925S3  
AC Q925S3;

DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE MRP3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
Su C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving  
the repair of intestinal epithelium after irradiation in mice.";  
World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
of the irradiated mice by treatment with the intestinal RNA of mice of  
the same strain.";  
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
RL EMBL; AF240166; AAK43731.1; -;  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;  
Query Match 66.0%; Score 62; DB 11; Length 147;  
Best Local Similarity 68.8%; Pred. No. 0.025;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 2 IYPGSGSAYYNEFK 17  
Db :||||| ||| |||  
53 IFPGGSTEYNEKFG 68  
RESULT 8  
Q8VDC9 PRELIMINARY; PRT; 168 AA.  
ID Q8VDC9  
AC Q8VDC9;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Anti-MOG Z12 variable gamma 2a (Fragment).  
GN IGG2A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Chernajovsky Y.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Sembi P.;  
RT "Targeting T cells to the CNS.";  
Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ416332; CAC94867.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR001230; Prenyl\_site.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00294; PRENYLATION; UNKNOWN\_1.  
FT NON\_TER 168

SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match 66.08; Score 62; DB 11; Length 168;  
Best Local Similarity 70.68; Pred. No. 0.029;  
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYYNEMFKG 17

||| ||| ||| |||

Db 69 E1LPGSGRTYNEKFKG 85

RESULT 9

Q9JL77 ID Q9JL77 PRELIMINARY; PRT; 110 AA.

AC Q9JL77

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Anti-myosin immunoglobulin heavy chain variable region

DE (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2;

RX MEDLINE=20448942; PubMed=10992488;

RA Markiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-Cell-dependent antibody response to the dominant epitope of

streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive

with cardiac myosin."

RL Infect. Immun. 68:5803-5808(2000).

DR EMBL; AF206029; AAF69327.1; -

DR HSSP; P01810; 2FBJ.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

FT NON\_TER 1 110

FT NON\_TER 110 110

SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match

Best Local Similarity 62.8%; Score 59; DB 11; Length 110;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 E1YPGSGSAYYNEMFKG 17

||| ||| ||| |||

42 E1HPNSGHTYNEKFKG 58

RESULT 10

Q9JL25 ID Q9JL25 PRELIMINARY; PRT; 473 AA.

AC Q9JL25

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Similar to RIKEN cdna 181060009 gene.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003888; AA003888.1; -

DR HSSP; P01842; 7FAB.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003597; Ig\_cl.

DR InterPro; IPR003600; Ig\_like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG\_like; 1.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match

Best Local Similarity 61.7%; Score 58; DB 11; Length 473;

Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17

||| ||| ||| |||

Db 70 IYPRDGSRTYNEKFKG 85

RESULT 11

Q9D9B8

ID Q9D9B8 PRELIMINARY; PRT; 111 AA.

AC Q9D9B8

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Adult male testis cDNA, RIKEN full-length enriched library,

clone:170011011, full insert sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TESTIS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Flutschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrini L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK007163; BAB24877.1; -

DR HSSP; P01810; 2FBJ.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003600; Ig\_like.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00406; IGV; 1.

DR SMART; SM00410; IG\_like; 1.

SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match

Best Local Similarity 58.5%; Score 55; DB 11; Length 111;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IYPGSGSAYYNEMFKG 17

KW Complete proteome.  
SQ SEQUENCE 335 AA; 38222 MW; 653D1AA484DC9FE3 CRC64;  
Query Match 53.2%; Score 50; DB 16; Length 335;  
Best Local Similarity 60.0%; Pred. No. 5.5; Mismatches 1; Indels 0; Gaps 0;  
Matches 9; Conservative 1;  
Oy 3 YPGSGSAYNEMFKG 17  
Db 284 YPGISLLYNAFTG 298  
PRT: 121 AA.  
PRELIMINARY:  
ID Q8YL22  
AC Q8YL22  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical protein All7116.  
DE Hypothetical protein All7116.  
GN AL17116.  
OS Anabaena sp. (strain PCC 7120).  
OG Plasmid pCC7120alpha.  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
RT cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
DR EMBL; AF003600; BAB78200.1; -  
KW Plasmid; Hypothetical protein; Complete proteome.  
SQ SEQUENCE 121 AA; 13184 MW; 79E76CFB575E96E3 CRC64;  
Query Match 51.1%; Score 48; DB 16; Length 121;  
Best Local Similarity 43.8%; Pred. No. 3.8;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
Oy 1 E1YPGSGSAYNEMFK 16  
Db 103 QVYPGNKDAYENTLAK 118  
PRT: 372 AA.  
PRELIMINARY:  
ID Q9F6B4  
AC Q9F6B4  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Surface-exposed lipoprotein.  
GN JLP4.  
OS Campylobacter jejuni.  
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
OC Campylobacter.  
OX NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21150466; PubMed=11251839;  
RA Jin S., Joe A., Lynett J., Hani E.K., Sherman P., Chan V.L.;  
RT "JlpA, a novel surface-exposed lipoprotein specific to Campylobacter  
RT jejuni, mediates adherence to host epithelial cells.";  
RL Mol. Microbiol. 39:1225-1236(2001).  
DR EMBL; AF295104; AAG29817.1; -  
KW Lipoprotein.  
SQ SEQUENCE 372 AA; 42290 MW; 695CDB8E4D2F1116 CRC64;  
Query Match 53.2%; Score 50; DB 11; Length 118;  
Best Local Similarity 50.0%; Pred. No. 1.7;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
Oy 2 IYPGSGSAYNEMFKG 17  
Db 51 IYPGSGDTSTQKFRG 66  
PRT: 335 AA.  
PRELIMINARY:  
ID Q9WXS7  
AC Q9WXS7  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE Oligopeptide ABC transporter, permease protein.  
GN TM0072.  
OS Thermotoga maritima.  
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.  
OX NCBI\_TaxID=2336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MSB / DSM 3109;  
RX MEDLINE=99287316; PubMed=10360571;  
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,  
RA Nelson K.E., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,  
RA McDonald L., Utterback T.R., Matk J.A., Linher K.D., Garrett M.M.,  
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,  
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;  
RT "Evidence for lateral gene transfer between Archaea and Bacteria from  
RT genome sequence of Thermotoga maritima.";  
RL Nature 399:323-329(1999).  
DR EMBL; AE001694; AAD35166.1; -  
DR TIGR; TM0072; -  
DR InterPro; IPR000515; BPD\_transp.  
DR Pfam; PF00528; BPD\_transp; 1.

Query Match 51.1%; Score 48; DB 2; Length 372;  
 Best Local Similarity 45.5%; Pred. No. 13;  
 Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 1;

QY 1 EYPPGSGSA-----YYNEMFK 16  
 ||| | :| ||| :||  
 Db 100 EYKGEANASISIKYNDLFK 121

Search completed: February 14, 2003, 11:18:37  
 Job time : 36.5376 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run On: February 14, 2003, 11:04:17 ; Search time 24.3871 Seconds  
(without alignments)  
49.176 Million cell updates/sec

Title: US-09-701-001b-3  
Perfect score: 50  
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
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11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
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13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 50    | 100.0       | 9      | AAV59258 | Antibody 4H5 H cha |
| 2          | 50    | 100.0       | 9      | AAV51135 | Murine CD4/CD34 re |
| 3          | 50    | 100.0       | 110    | AAV59262 | Antibody 4H5 H cha |
| 4          | 50    | 100.0       | 110    | AAV51139 | Murine derived pro |
| 5          | 50    | 100.0       | 118    | AAV59266 | Antibody 4H5 H cha |
| 6          | 50    | 100.0       | 118    | AAV51143 | Murine derived pro |
| 7          | 50    | 100.0       | 118    | AAV51145 | Murine derived pro |
| 8          | 50    | 100.0       | 305    | AAV59264 | Antibody 4H5 H cha |
| 9          | 50    | 100.0       | 305    | AAV59265 | Antibody 4H5 L cha |
| 10         | 50    | 100.0       | 305    | AAV51141 | Murine derived pro |

|    |    |       |     |    |          |                    |
|----|----|-------|-----|----|----------|--------------------|
| 11 | 50 | 100.0 | 305 | 21 | AAV51142 | Murine derived pro |
| 12 | 44 | 88.0  | 20  | 23 | AAU70801 | Hepatitis B virus  |
| 13 | 44 | 88.0  | 130 | 23 | AAU70768 | Hepatitis B virus  |
| 14 | 40 | 80.0  | 122 | 11 | AAU04135 | Anti-Leu 3a heavy  |
| 15 | 40 | 80.0  | 136 | 11 | AAU04133 | Anti-Leu 3a heavy  |
| 16 | 39 | 78.0  | 176 | 22 | AAU19301 | Human G protein-co |
| 17 | 37 | 74.0  | 21  | 21 | AAV51684 | Murine clodin 3 pr |
| 18 | 37 | 74.0  | 219 | 21 | AAV51679 | Murine clodin 3 pr |
| 19 | 37 | 74.0  | 266 | 22 | AAU60366 | zebrafish atonal h |
| 20 | 36 | 72.0  | 150 | 23 | ABU77826 | Amino acid sequenc |
| 21 | 35 | 70.0  | 145 | 20 | AAU48329 | Human prostate can |
| 22 | 35 | 70.0  | 177 | 22 | AAU67760 | Propionibacterium  |
| 23 | 35 | 70.0  | 277 | 20 | AAU96343 | SfVHC-1-8k single  |
| 24 | 35 | 70.0  | 338 | 23 | ABU41394 | Human ovarian anti |
| 25 | 35 | 70.0  | 439 | 22 | ABU76766 | Corynebacterium gl |
| 26 | 35 | 70.0  | 448 | 22 | AAU93041 | C glutamic prote   |
| 27 | 35 | 70.0  | 576 | 21 | AAU54335 | Human pancreatic c |
| 28 | 35 | 70.0  | 579 | 14 | AAU34446 | N.meningitidis 239 |
| 29 | 35 | 70.0  | 579 | 14 | AAU34401 | Sequence of low mo |
| 30 | 35 | 70.0  | 640 | 20 | AAU39926 | Bovine rotavirus S |
| 31 | 35 | 70.0  | 789 | 23 | ABU05687 | Human differentiat |
| 32 | 34 | 68.0  | 94  | 22 | AAU83608 | Human immune/haema |
| 33 | 34 | 68.0  | 105 | 21 | AAU20186 | Arabidopsis thalia |
| 34 | 34 | 68.0  | 105 | 21 | AAU20185 | Arabidopsis thalia |
| 35 | 34 | 68.0  | 134 | 21 | AAU20185 | Arabidopsis thalia |
| 36 | 34 | 68.0  | 134 | 21 | AAU47231 | Arabidopsis thalia |
| 37 | 34 | 68.0  | 163 | 21 | AAU38045 | Fragment of human  |
| 38 | 34 | 68.0  | 251 | 20 | AAU88496 | Human stomach canc |
| 39 | 34 | 68.0  | 251 | 21 | AAU41852 | Human ORFX ORF1616 |
| 40 | 34 | 68.0  | 251 | 21 | AAU66632 | Membrane-bound pro |
| 41 | 34 | 68.0  | 251 | 22 | AAU29024 | Human PRO polypept |
| 42 | 34 | 68.0  | 251 | 22 | AAU78501 | Human protein SEQ  |
| 43 | 34 | 68.0  | 251 | 22 | AAU65155 | Human PRO276 (UNQ2 |
| 44 | 34 | 68.0  | 277 | 19 | AAU85849 | S. pneumoniae deri |
| 45 | 34 | 68.0  | 279 | 20 | AAU60100 | Human endometrium  |

## ALIGNMENTS

RESULT 1  
AAV59258  
ID AAV59258 standard; peptide; 9 AA.  
XX  
AC AAV59258;  
XX  
DT 17-APR-2000 (first entry)  
XX  
DE Antibody 4H5 H chain variable region CDR3 fragment.  
XX  
KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;  
KW complementarity determining region.  
XX  
OS Mus sp.  
XX  
PN JP1132563-A.  
XX  
PD 07-DEC-1999.  
XX  
PF 26-MAY-1998; 98JP-0163034.  
XX  
PR 26-MAY-1998; 98JP-0163034.  
XX  
PA (ASAH ) ASAH KASEI KOGYO KK.  
XX  
DR WPI; 2000-091351/08.  
XX  
PT An antibody and the nucleic acid coding the antibody -  
XX  
PS Claim 1; Page 14; 25pp; Japanese.  
XX  
CC The invention provides an antibody having affinity to CD4 antigen. The  
anti-human CD4 antibody 4H5 is used for the detection of antigen and

CC application for drugs. It is highly safe in human dose. Sequences  
 CC AAY59256-58 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the H chain variable region of the  
 CC antibody 4H5 respectively.  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
 |||||  
 Db 1 RGTGTGFAY 9

RESULT 2

AAY51135  
 XX AAY51135 standard; Protein; 9 AA.  
 AC AAY51135;

31-MAR-2000 (first entry)

DE Murine CD4/CD34 recognizing antibody heavy chain CDR-3 region #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; complementarity determining region;  
 KW CDR-3; heavy chain; murine.  
 XX

OS Mus sp.

XX WO9961629-A1.  
 PN  
 XX

PD 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

PR 26-MAY-1998; 98JP-0163023.

XX (ASAH ) ASahi KASEI KOGYO KK.

PA (ASAH ) ASahi MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI; 2000-086720/07.

DR Devices containing antibodies recognising CD4 or CD34 and their use for  
 XX the separation of CD4 or CD34 positive cells -

PS Claim 3; Page 76; 11pp; Japanese.

CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived complementarity determining  
 CC region CDR-3 protein fragment which is used to illustrate the method of  
 CC the invention.  
 XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

Db 1 RGTGTGFAY 9

RESULT 3

AAY59262

XX AAY59262 standard; Protein; 110 AA.

AC AAY59262;

XX 17-APR-2000 (first entry)

XX Antibody 4H5 H chain variable region.

XX CD4 antigen; anti-human; antibody; 4H5; drug.

OS Mus sp.

XX JP11332563-A.

XX 07-DEC-1999.

XX 26-MAY-1998; 98JP-0163034.

XX 26-MAY-1998; 98JP-0163034.

XX (ASAH ) ASahi KASEI KOGYO KK.

XX WPI; 2000-091351/08.

DR N-PSDB; AAZ58661.

XX An antibody and the nucleic acid coding the antibody -

XX Claim 5; Page 15; 25pp; Japanese.

CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain variable region of the antibody 4H5.

SQ Sequence 110 AA;

Query Match 100.0%; Score 50; DB 21; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

Db 91 RGTGTGFAY 99

RESULT 4

AAY51139

XX AAY51139 standard; Protein; 110 AA.

AC AAY51139;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #1.

XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX

OS Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

*put priority for withdrawal*



priority for student

ID AAY51145 standard; Protein: 118 AA.  
 AC AAY51145;  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 DE Murine derived protein fragment #7.  
 XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9961629-A1.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 24-MAY-1999; 99WO-JP02711.  
 XX  
 PR 25-MAY-1998; 98JP-0159957.  
 XX  
 PR 26-MAY-1998; 98JP-0163023.  
 XX  
 (ASAH ) ASAH KASEI KOGYO KK.  
 (ASAH ) ASAH MEDICAL CO LTD.  
 PA  
 PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX  
 DR WPI; 2000-086720/07.  
 DR N-PSDB; AAZ44231.  
 XX  
 PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 XX Disclosure; Page 96-97; 111pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 SQ Sequence 118 AA;  
 Query Match 100.0%; Score 50; DB 21; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGTGTGFAY 9  
 DB 99 RGTGTGFAY 107  
 RESULT 8  
 AAY59264  
 ID AAY59264 standard; protein; 305 AA.  
 XX  
 AC AAY59264;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 DE Antibody 4H5 H chain sequence.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 DR N-PSDB; AAZ58664.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 XX  
 PS Disclosure; Page 17-18; 25pp; Japanese.  
 XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the L chain sequence of the antibody 4H5.  
 XX  
 SQ Sequence 305 AA;  
 Query Match 100.0%; Score 50; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 DR N-PSDB; AAZ58663.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 XX  
 PS Disclosure; Page 16-17; 25pp; Japanese.  
 XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain sequence of the antibody 4H5.  
 XX  
 SQ Sequence 305 AA;  
 Query Match 100.0%; Score 50; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGTGTGFAY 9  
 DB 247 RGTGTGFAY 255  
 RESULT 9  
 AAY59265  
 ID AAY59265 standard; protein; 305 AA.  
 XX  
 AC AAY59265;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 DE Antibody 4H5 L chain sequence.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 DR N-PSDB; AAZ58664.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 XX  
 PS Disclosure; Page 17-18; 25pp; Japanese.  
 XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the L chain sequence of the antibody 4H5.  
 XX  
 SQ Sequence 305 AA;  
 Query Match 100.0%; Score 50; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGTGTGFAY 9  
|||||  
Db 121 RGTGTGFAY 129

RESULT 10  
AA51141  
ID AA51141 standard; Protein; 305 AA.  
XX AC  
XX AC  
XX AAY51141;  
XX  
XX  
XX 31-MAR-2000 (first entry)  
XX  
XX  
XX Murine derived protein fragment #3.

Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
HIV infection; autoimmune disease; murine.

Mus sp.  
WO9961629-A1.  
02-DEC-1999.

24-MAY-1999; 99WO-JP02711.  
25-MAY-1998; 98JP-0159957.  
26-MAY-1998; 98JP-0163023.  
XX (ASAH ) ASAH KASEI KOGYO KK.  
PA (ASAH ) ASAH KASEI KOGYO KK LTD.  
XX  
XX Ono M, Soka T, Morimoto I, Miyamura K;  
XX  
XX WPI; 2000-086720/07.  
XX N-PSDB; AA244206.

Devices containing antibodies recognising CD4 or CD34 and their use for  
the separation of CD4 or CD34 positive cells -

Claim 22; Page 80-82; 111pp; Japanese.

This invention describes a novel device (I) for separating cluster  
differentiation (CD)-positive cells using a recombinant (chimeric or  
single-chain) antibody recognising CD4 or CD34. The devices are useful  
for the separation of CD4 or CD34 positive cells, which is useful for  
the collection of hematopoietic undifferentiated cells, elimination of  
lymphocytes from cells to be used in bone marrow transplantation, the  
detection of leukemic cells and the production of medicinal  
compositions for the treatment of HIV infection and autoimmune diseases.  
This sequence represents a murine derived protein fragment which is used  
to illustrate the method of the invention.

Sequence 305 AA;

Query Match 100.0%; Score 50; DB 21; Length 305;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGTGTGFAY 9  
|||||  
Db 247 RGTGTGFAY 255

RESULT 11  
AAY51142  
ID AAY51142 standard; Protein; 305 AA.  
XX AC  
XX AAY51142;  
XX  
XX 31-MAR-2000 (first entry)  
DT

XX

Murine derived protein fragment #4.

DE

Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
HIV infection; autoimmune disease; murine.

OS

Mus sp.

WO9961629-A1.

02-DEC-1999.

24-MAY-1999; 99WO-JP02711.

25-MAY-1998; 98JP-0159957.

26-MAY-1998; 98JP-0163023.

XX (ASAH ) ASAH KASEI KOGYO KK.

PA (ASAH ) ASAH KASEI KOGYO KK LTD.

XX

Ono M, Soka T, Morimoto I, Miyamura K;

XX

WPI; 2000-086720/07.

XX N-PSDB; AA244206.

XX

Devices containing antibodies recognising CD4 or CD34 and their use for

the separation of CD4 or CD34 positive cells -

Claim 22; Page 82-84; 111pp; Japanese.

XX

This invention describes a novel device (I) for separating cluster

differentiation (CD)-positive cells using a recombinant (chimeric or

single-chain) antibody recognising CD4 or CD34. The devices are useful

for the separation of CD4 or CD34 positive cells, which is useful for

the collection of hematopoietic undifferentiated cells, elimination of

lymphocytes from cells to be used in bone marrow transplantation, the

detection of leukemic cells and the production of medicinal

compositions for the treatment of HIV infection and autoimmune diseases.

This sequence represents a murine derived protein fragment which is used

to illustrate the method of the invention.

XX

Sequence 305 AA;

Query Match 100.0%; Score 50; DB 21; Length 305;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RGTGTGFAY 9

|||||

Db 121 RGTGTGFAY 129

RESULT 12

AAU70801

ID AAU70801 standard; Peptide; 20 AA.

XX

AAU70801;

XX

14-FEB-2002 (first entry)

XX

Hepatitis B virus antigen binding partner #33.

XX

Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;

anti-inflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;

B cell mediated processing; T cell proliferation; cytokine production;

immune system response.

XX

Synthetic.

XX

WO200181421-A2.

XX

01-NOV-2001.

PD

*pcr priority for  
instead*

XX 20-APR-2001; 2001WO-IB00844.  
 XX PF  
 XX 21-APR-2000; 2000US-0556605.  
 XX PI  
 XX (TRIP-) TRIPEP AB.  
 XX PA  
 XX Sallberg M;  
 XX PI  
 XX WPI; 2002-055347/07.  
 XX DR  
 XX Novel peptide that binds to hepatitis B virus core or E antigen, useful  
 XX PT for treating and preventing hepatitis B virus infection  
 XX PS  
 XX Claim 2; Page 33; 82pp; English.  
 XX CC  
 XX The invention relates to an isolated or purified peptide (I) which binds  
 XX CC Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).  
 XX CC (I) is useful for treating or preventing Hepatitis B virus (HBV)  
 XX CC infection, by identifying a subject in need of a molecule that inhibits  
 XX CC HBV infection, and providing the subject with (I). (I) is also useful  
 XX CC for determining the presence of HBV in a biological sample, and for  
 XX CC inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,  
 XX CC by determining whether (I) inhibits B cell mediated processing and  
 XX CC uptake of HBcAg and/or HBeAg by performing an assay of T cell  
 XX CC proliferation or cytokine production. (I) is also useful for modulating  
 XX CC an immune system response. (I) is useful as a template for a design of  
 XX CC synthetic molecules including peptides, derivatives or modified peptides,  
 XX CC peptidomimetics and chemicals. (I) is also useful as biotechnological  
 XX CC tool, diagnostic reagent and as active ingredient in pharmaceuticals.  
 XX CC (I) is also useful as detection reagents in conventional  
 XX CC immunohistochemical techniques, as diagnostic reagents to detect HBV in  
 XX CC biological sample, and to determine the efficacy of an HBV treatment  
 XX CC protocol by monitoring the levels of HBcAg and/or HBeAg during and after  
 XX CC treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core  
 XX CC antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described  
 XX CC in the invention.  
 XX SQ Sequence 20 AA;  
 Query Match 88.0%; Score 44; DB 23; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 0.8;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RGTGTGFAY 9  
 DB 7 RGKGTGFAY 15  
 RESULT 13  
 AAU70768  
 AAU70768 standard; Peptide; 130 AA.  
 XX AC AAU70768;  
 XX 14-FEB-2002 (first entry)  
 XX DT  
 XX Hepatitis B virus antigen binding partner 9C8 VH.  
 XX DE  
 XX Hepatitis B virus; virucide; immunomodulator; hepatotropic; HBV;  
 XX KW antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;  
 XX KW B cell mediated processing; T cell proliferation; cytokine production;  
 XX KW immune system response.  
 XX OS Synthetic.  
 XX WO200181421-A2.  
 XX 01-NOV-2001.  
 XX 20-APR-2001; 2001WO-IB00844.  
 XX PF  
 XX 21-APR-2000; 2000US-0556605.  
 XX / PR

XX (TRIP-) TRIPEP AB.  
 XX PI  
 XX Sallberg M;  
 XX WPI; 2002-055347/07.  
 XX DR  
 XX Novel peptide that binds to hepatitis B virus core or E antigen, useful  
 XX PT for treating and preventing hepatitis B virus infection  
 XX PS  
 XX Claim 2; Page 11; 82pp; English.  
 XX CC  
 XX The invention relates to an isolated or purified peptide (I) which binds  
 XX CC Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).  
 XX CC (I) is useful for treating or preventing Hepatitis B virus (HBV)  
 XX CC infection, by identifying a subject in need of a molecule that inhibits  
 XX CC HBV infection, and providing the subject with (I). (I) is also useful  
 XX CC for determining the presence of HBV in a biological sample, and for  
 XX CC inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,  
 XX CC by determining whether (I) inhibits B cell mediated processing and  
 XX CC uptake of HBcAg and/or HBeAg by performing an assay of T cell  
 XX CC proliferation or cytokine production. (I) is also useful for modulating  
 XX CC an immune system response. (I) is useful as a template for a design of  
 XX CC synthetic molecules including peptides, derivatives or modified peptides,  
 XX CC peptidomimetics and chemicals. (I) is also useful as biotechnological  
 XX CC tool, diagnostic reagent and as active ingredient in pharmaceuticals.  
 XX CC (I) is also useful as detection reagents in conventional  
 XX CC immunohistochemical techniques, as diagnostic reagents to detect HBV in  
 XX CC biological sample, and to determine the efficacy of an HBV treatment  
 XX CC protocol by monitoring the levels of HBcAg and/or HBeAg during and after  
 XX CC treatment. AAU70766-AAU70876 represent Hepatitis B virus (HBV) core  
 XX CC antigen (HBcAg) or HBV E antigen (HBeAg) binding partners as described  
 XX CC in the invention.  
 XX SQ Sequence 130 AA;  
 Query Match 88.0%; Score 44; DB 23; Length 130;  
 Best Local Similarity 88.9%; Pred. No. 4.9;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 RGTGTGFAY 9  
 DB 97 RGKGTGFAY 105  
 RESULT 14  
 AAR04135  
 ID AAR04135 standard; protein; 122 AA.  
 XX AC AAR04135;  
 XX 06-SEP-1990 (first entry)  
 XX DT  
 XX Anti-Leu 3a heavy chain variable region gene product, KOL/316 VH.  
 XX DE  
 XX HIV; AIDS; anti-Leu3A; vaccine; ds.  
 XX KW  
 XX Mus musculus.  
 XX OS  
 XX EP365209-A.  
 XX PN  
 XX 25-APR-1990.  
 XX PD  
 XX 11-OCT-1989; 89EP-0010415.  
 XX PF  
 XX 17-OCT-1988; 88US-0260558.  
 XX PR  
 XX (BECT ) BECTON DICKINSON CO.  
 XX PA  
 XX Hinton R, Oi VT;  
 XX PI  
 XX WPI; 1990-126329/17.  
 XX DR  
 XX N-PSDB; AAQ04042.

Fri Feb 14 15:00:52 2003

XX New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.  
XX  
XX Claim 5; Fig 5; 12pp; English.  
XX  
XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.  
XX  
SQ Sequence 122 AA;

Query Match 80.0%; Score 40; DB 11; Length 122;  
Best Local Similarity 77.8%; Pred. No. 21;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
|||  
103 RGKGTGFAY 111

RESULT 15  
AAR04133  
ID AAR04133 standard; protein; 136 AA.

XX AAR04133;  
XX  
XX 06-SEP-1990 (first entry)  
XX  
XX Anti-Leu 3a heavy chain variable region gene product, 316 Vh.  
XX  
XX HIV; AIDS; anti-Leu3A; vaccine; ds.

XX Mus musculus.  
XX  
XX EP365209-A.  
XX  
XX 25-APR-1990.

XX 11-OCT-1989; 89EP-0N10415.

XX 17-OCT-1988; 88US-0260558.

XX (BECT ) BECTON DICKINSON CO.

XX Hinton R, Oi VT;

DR WPI; 1990-126329/17.  
N-PSDB; AAQ04040.

XX New chimeric variants of murine antibody anti-leucine -  
PT contg. human antibody regions, and DNA encoding sequences.

XX Claim 2; Fig 3; 12pp; English.

XX Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be  
CC used to form chimeric mouse-variable, human-constant region Abs  
CC suggested as being useful as a vaccine to HIV.

XX Sequence 136 AA;

Query Match 80.0%; Score 40; DB 11; Length 136;  
Best Local Similarity 77.8%; Pred. No. 24;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
|||  
Db 117 RGKGTGFAY 125

Search completed: February 14, 2003, 11:15:43  
Job time : 25.3871 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 ; Search time 8.12903 Seconds  
(without alignments)  
32.575 Million cell updates/sec

Title: US-09-701-001b-3  
Perfect score: 50  
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA: \*  
1: /cgn2.6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2.6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2.6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2.6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2.6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 44    | 88.0        | 20     | 4     | US-09-556-605-36  |
| 2          | 44    | 88.0        | 130    | 4     | US-09-556-605-3   |
| 3          | 37    | 74.0        | 247    | 4     | US-09-130-491-15  |
| 4          | 35    | 70.0        | 579    | 1     | US-08-064-174-1   |
| 5          | 35    | 70.0        | 579    | 1     | US-08-066-167-1   |
| 6          | 35    | 70.0        | 579    | 2     | US-08-449-733-1   |
| 7          | 35    | 70.0        | 640    | 2     | US-08-671-978A-10 |
| 8          | 34    | 68.0        | 20     | 4     | US-09-314-242-10  |
| 9          | 34    | 68.0        | 251    | 2     | US-08-933-750C-44 |
| 10         | 34    | 68.0        | 251    | 4     | US-09-234-613-44  |
| 11         | 34    | 68.0        | 280    | 1     | US-08-434-255-8   |
| 12         | 34    | 68.0        | 280    | 1     | US-08-459-967-8   |
| 13         | 34    | 68.0        | 280    | 1     | US-08-460-327-8   |
| 14         | 34    | 68.0        | 280    | 1     | US-08-459-871-8   |
| 15         | 34    | 68.0        | 280    | 4     | US-09-024-532-2   |
| 16         | 34    | 68.0        | 280    | 4     | US-09-104-623A-2  |
| 17         | 34    | 68.0        | 280    | 4     | US-09-019-532-2   |
| 18         | 34    | 68.0        | 280    | 4     | US-09-417-359A-2  |
| 19         | 34    | 68.0        | 370    | 1     | US-08-434-255-6   |
| 20         | 34    | 68.0        | 370    | 1     | US-08-459-967-6   |
| 21         | 34    | 68.0        | 370    | 1     | US-08-460-327-6   |
| 22         | 34    | 68.0        | 370    | 1     | US-08-459-871-6   |
| 23         | 34    | 68.0        | 397    | 1     | US-08-434-255-2   |
| 24         | 34    | 68.0        | 397    | 1     | US-08-434-255-4   |
| 25         | 34    | 68.0        | 397    | 1     | US-08-459-967-2   |
| 26         | 34    | 68.0        | 397    | 1     | US-08-459-967-4   |
| 27         | 34    | 68.0        | 397    | 1     | US-08-460-327-2   |

|    |      |      |      |   |                     |                    |
|----|------|------|------|---|---------------------|--------------------|
| 28 | 34   | 68.0 | 397  | 1 | US-08-460-327-4     | Sequence 4, Appli  |
| 29 | 34   | 68.0 | 397  | 1 | US-08-459-871-2     | Sequence 2, Appli  |
| 30 | 34   | 68.0 | 397  | 1 | US-08-459-871-4     | Sequence 4, Appli  |
| 31 | 34   | 68.0 | 1394 | 4 | US-08-296-791-2     | Sequence 2, Appli  |
| 32 | 34   | 68.0 | 1394 | 5 | PCT-US95-10661A-2   | Sequence 2, Appli  |
| 33 | 33   | 66.0 | 272  | 4 | US-09-134-001C-4238 | Sequence 4238, Ap  |
| 34 | 33   | 66.0 | 445  | 4 | US-08-887-534A-61   | Sequence 61, Appli |
| 35 | 32   | 64.0 | 348  | 4 | US-09-113-536-2     | Sequence 2, Appli  |
| 36 | 32   | 64.0 | 348  | 4 | US-09-624-183-2     | Sequence 2, Appli  |
| 37 | 32   | 64.0 | 348  | 5 | PCT-US95-05785-2    | Sequence 2, Appli  |
| 38 | 32   | 64.0 | 461  | 2 | US-08-630-822A-68   | Sequence 68, Appli |
| 39 | 32   | 64.0 | 461  | 2 | US-09-005-069-68    | Sequence 68, Appli |
| 40 | 32   | 64.0 | 461  | 4 | US-09-171-156A-27   | Sequence 27, Appli |
| 41 | 32   | 64.0 | 659  | 4 | US-09-562-737-18    | Sequence 18, Appli |
| 42 | 31.5 | 63.0 | 1130 | 2 | US-08-460-309-2     | Sequence 2, Appli  |
| 43 | 31.5 | 63.0 | 1130 | 2 | US-08-125-077-2     | Sequence 2, Appli  |
| 44 | 31.5 | 63.0 | 1130 | 6 | 5444158-2           | Patent No. 5444158 |
| 45 | 31.5 | 63.0 | 3111 | 2 | US-08-460-309-4     | Sequence 4, Appli  |

ALIGNMENTS

RESULT 1  
US-09-556-605-36  
; Sequence 36, Application US/09556605  
; Patent No. 6417324  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; APPLICANT: Lazdina, Una  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP.020A  
; CURRENT APPLICATION NUMBER: US/09/556.605  
; CURRENT FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Oligonucleotide  
US-09-556-605-36

Query Match 88.0% Score 44; DB 4; Length 20;  
Best Local Similarity 88.9% Pred. No. 0.29;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGTGTGFAY 9  
Db 7 RGKGTGFAY 15

RESULT 2  
US-09-556-605-3  
; Sequence 3, Application US/09556605  
; Patent No. 6417324  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; APPLICANT: Lazdina, Una  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP.020A  
; CURRENT APPLICATION NUMBER: US/09/556.605  
; CURRENT FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Artificial Oligonucleotide  
US-09-556-605-3

Query Match 88.0%; Score 44; DB 4; Length 130;

Best Local Similarity 88.9%; Pred. No. 1.8; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

Db 97 RKGTTGFAY 105

RESULT 3

US-09-130-491-15

; Sequence 15, Application US/09130491

; Patent No. 6416974

; GENERAL INFORMATION:

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Goodearl, Andrew D.J.

; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83

; CURRENT APPLICATION NUMBER: US/09130491

; CURRENT FILING DATE: 1998-08-07

; EARLIER APPLICATION NUMBER: US 60/058,108

; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: US 60/054,961

; EARLIER FILING DATE: 1997-08-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 247

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-130-491-15

Query Match

Best Local Similarity 74.0%; Score 37; DB 4; Length 247;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTGTGFAY 9

Db 205 GGTGTGFAY 212

RESULT 4

US-08-064-174-1

; Sequence 1, Application US/08064174

; Patent No. 5618540

; GENERAL INFORMATION:

; APPLICANT: QUENTIN-MILLET, Marie-Jose

; APPLICANT: LISSOLO, Ling

; TITLE OF INVENTION: SUBUNIT VACCINE FOR NEISSERIA

; TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED

; TITLE OF INVENTION: SUBUNITS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: George Mason Bldg., Washington & Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/064,174

; FILING DATE: 25-MAY-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 12176

; FILING DATE: 03-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016100-001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703/836-6620

; TELEFAX: 703/836-2021

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 579 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-064-174-1

Query Match

Best Local Similarity 70.0%; Score 35; DB 1; Length 579;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9

Db 442 RGTGTGFAY 450

RESULT 5

US-08-066-167-1

; Sequence 1, Application US/08066167

; Patent No. 5618541

; GENERAL INFORMATION:

; APPLICANT: QUENTIN-MILLET, Marie-Jose

; TITLE OF INVENTION: VACCINE AGAINST NEISSERIA MENINGITIDIS

; TITLE OF INVENTION: INFECTIONS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: George Mason Bldg., Washington & Prince Sts.

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/066,167

; FILING DATE: 02-JUN-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 12177

; FILING DATE: 03-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Crane-Feury, Sharon E

; REGISTRATION NUMBER: 36,113

; REFERENCE/DOCKET NUMBER: 016100-002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 579 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Neisseria meningitidis 2394 subunit rbp2.

US-08-066-167-1

Query Match

Best Local Similarity 70.0%; Score 35; DB 1; Length 579;



Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
||||| : |  
Db 442 RGTGTWGY 450

RESULT 6  
US-08-449-733-1  
; Sequence 1, Application US/08449733  
; Patent No. 5928650  
; GENERAL INFORMATION:  
; APPLICANT: QUENTIN-MILLET, Marie-Jose  
; APPLICANT: LISSOLO, Ling  
; TITLE OF INVENTION: SUBUNIT VACCINE FOR NEISSERIA  
; TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED  
; TITLE OF INVENTION: SUBUNITS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,733  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 12176  
; FILING DATE: 03-OCT-1991  
; APPLICATION DATA: 08/064,174  
; FILING DATE: 25-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McGowan, Malcolm K.  
; REGISTRATION NUMBER: 39,300  
; REFERENCE/DOCKET NUMBER: 016100-006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703/836-6620  
; TELEFAX: 703/836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-449-733-1

Query Match 70.0%; Score 35; DB 2; Length 579;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
||||| : |  
Db 442 RGTGTWGY 450

RESULT 7  
US-08-671-978A-10  
; Sequence 10, Application US/08671978A  
; Patent No. 5959093  
; GENERAL INFORMATION:  
; APPLICANT: Saif, Linda J.  
; APPLICANT: Parwani, Anil

Query Match 68.0%; Score 34; DB 4; Length 20;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFA 8  
||| ||:|

Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
||||| : |  
Db 442 RGTGTWGY 450

RESULT 6  
US-08-449-733-1  
; Sequence 1, Application US/08449733  
; Patent No. 5928650  
; GENERAL INFORMATION:  
; APPLICANT: QUENTIN-MILLET, Marie-Jose  
; APPLICANT: LISSOLO, Ling  
; TITLE OF INVENTION: SUBUNIT VACCINE FOR NEISSERIA  
; TITLE OF INVENTION: MENINGITIDIS INFECTIONS AND CORRESPONDING PURIFIED  
; TITLE OF INVENTION: SUBUNITS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/671,978A  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GOLTRICK, MARY E  
; REGISTRATION NUMBER: 34,829  
; REFERENCE/DOCKET NUMBER: 22727/00133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 622-8200  
; TELEFAX: (216) 241-0816  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 640 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-671-978A-10

Query Match 70.0%; Score 35; DB 2; Length 640;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
:|||||  
Db 451 SGTGFAY 457

RESULT 8  
US-09-314-242-10  
; Sequence 10, Application US/09314242A  
; Patent No. 6248575  
; GENERAL INFORMATION:  
; APPLICANT: Elizabeth J. Golightly  
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides  
; FILE REFERENCE: 5556.200-US  
; CURRENT APPLICATION NUMBER: US/09/314,242A  
; EARLIER FILING DATE: 1999-05-18  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Trichoderma harzianum  
US-09-314-242-10

Query Match 68.0%; Score 34; DB 4; Length 20;  
Best Local Similarity 75.0%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFA 8  
||| ||:|

Db 3 RGTNTGYA 10

## RESULT 9

US-08-933-750C-44  
; Sequence 44, Application US/08933750C  
; Patent No. 5932442  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750C  
; FILING DATE: September 23, 1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: THPINOT03  
; CLONE: 2469611  
US-08-933-750C-44

Query Match 68.0%; Score 34; DB 2; Length 251;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9  
Db 65 GPGTGFLY 72

## RESULT 10

US-09-234-613-44  
; Sequence 44, Application US/09234613  
; Patent No. 6132973  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Bandman, Olga

; APPLICANT: Shah, Purvi  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Yue, Henry  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,613  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,750  
; FILING DATE: September 23, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0356 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 251 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: THPINOT03  
; CLONE: 2469611  
US-09-234-613-44

Query Match 68.0%; Score 34; DB 4; Length 251;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9  
Db 65 GPGTGFLY 72

## RESULT 11

US-08-434-255-8  
; Sequence 8, Application US/08434255  
; Patent No. 5621089  
; GENERAL INFORMATION:  
; APPLICANT: Sloma, Alan P.  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Dambmann, Claus  
; APPLICANT: Aaslyng, Dorrit  
; TITLE OF INVENTION: ALKALINE PROTEASE  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5621089o No. 5621089disk of No. 5621089th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:

Fri Feb 14 15:00:52 2003

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/434,255  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Agis Dr., Cheryl H.  
 ; REGISTRATION NUMBER: 34,086  
 ; REFERENCE/DOCKET NUMBER: 3764.400-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-867-0123  
 ; TELEFAX: 212-878-9655  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-434-255-8

Query Match 68.0%; Score 34; DB 1; Length 280;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
 Db 262 GTGTNFKY 269

RESULT 12  
 ; Sequence 8, Application US/08459967  
 ; Patent No. 5622841  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloma, Alan P.  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Dammann, Claus  
 ; APPLICANT: Aslyng, Dorrit  
 ; TITLE OF INVENTION: ALKALINE PROTEASE  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: No. 5622841o No. 5622841disk of No. 5622841th America, Inc.  
 ; STREET: 405 Lexington Avenue, 64th Floor  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10174-6401  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/459,967  
 ; FILING DATE: 02-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/434,255  
 ; FILING DATE: 03-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Agis Dr., Cheryl H.  
 ; REGISTRATION NUMBER: 34,086  
 ; REFERENCE/DOCKET NUMBER: 3764.400-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-867-0123  
 ; TELEFAX: 212-878-9655  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid

; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-459-967-8  
 Query Match 68.0%; Score 34; DB 1; Length 280;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
 Db 262 GTGTNFKY 269

RESULT 13  
 ; Sequence 8, Application US/08460327  
 ; Patent No. 5622850  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloma, Alan P.  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Dammann, Claus  
 ; APPLICANT: Aslyng, Dorrit  
 ; TITLE OF INVENTION: ALKALINE PROTEASE  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: No. 5622850o No. 5622850disk of No. 5622850th America, Inc.  
 ; STREET: 405 Lexington Avenue, 64th Floor  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10174-6401  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/460,327  
 ; FILING DATE: 02-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/434,255  
 ; FILING DATE: 03-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Agis Dr., Cheryl H.  
 ; REGISTRATION NUMBER: 34,086  
 ; REFERENCE/DOCKET NUMBER: 3764.400-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-867-0123  
 ; TELEFAX: 212-878-9655  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 280 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-460-327-8

Query Match 68.0%; Score 34; DB 1; Length 280;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
 Db 262 GTGTNFKY 269

RESULT 14  
 ; Sequence 8, Application US/08459871  
 ; Patent No. 5650326  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloma, Alan P.

;; APPLICANT: Outtrup, Helle  
;; APPLICANT: Dambmann, Claus  
;; APPLICANT: Aaslyng, Dorrit  
;; TITLE OF INVENTION: ALKALINE PROTEASE  
;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: No. 56503260 No. 5650326disk of No. 5650326th America, Inc.  
;; STREET: 405 Lexington Avenue, 64th Floor  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10174-6401  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/459,871  
;; FILING DATE: 02-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/434,255  
;; FILING DATE: 03-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Agri Dr. Cheryl H.  
;; REGISTRATION NUMBER: 34,086  
;; REFERENCE/DOCKET NUMBER: 3764.400-US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 212-867-0123  
;; TELEFAX: 212-878-9655  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 280 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-459-871-8

Query Match 58.0%; Score 34; DB 1; Length 280;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
|||||  
Db 262 GTGTNFKY 269

ILT 15

9-024-532-2  
; Sequence 2, Application US/09024532  
; Patent No. 6245901  
; GENERAL INFORMATION:  
; APPLICANT: von der Osten, Claus  
; APPLICANT: Olsen, Arne Agerlin  
; APPLICANT: Roggen, Erwin Ludo  
; TITLE OF INVENTION: A Modified Polypeptide  
; FILE REFERENCE: 4923.204-US  
; CURRENT APPLICATION NUMBER: US/09/024,532  
; CURRENT FILING DATE: 1998-02-17  
; EARLIER APPLICATION NUMBER: PCT/DK98/00046  
; EARLIER FILING DATE: 1998-02-06  
; EARLIER APPLICATION NUMBER: 0135/97  
; EARLIER FILING DATE: 1997-02-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: bacillus sp.  
US-09-024-532-2  
Query Match 68.0%; Score 34; DB 4; Length 280;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
|||||  
Db 262 GTGTNFKY 269

Search completed: February 14, 2003, 11:20:48  
Job time : 9.12903 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 5.22581 Seconds  
(without alignments)  
44.001 Million cell updates/sec

Title: US-09-701-001b-3

Perfect score: 50

Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

140259 seqs, 2554876 residues

1 number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### Database :

Published\_Applications\_AA:\*

- 1: /cgn2.6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2.6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2.6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2.6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2.6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2.6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2.6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2.6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2.6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2.6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2.6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2.6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2.6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2.6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description        |
|------------|-------|---------------|--------|-------|--------------------|
| 1          | 44    | 88.0          | 20     | 10    | US-09-839-447A-36  |
| 2          | 44    | 88.0          | 130    | 10    | US-09-839-447A-3   |
| 3          | 37    | 74.0          | 247    | 12    | US-10-105-929-15   |
| 4          | 37    | 74.0          | 248    | 9     | US-09-759-130B-137 |
| 5          | 37    | 74.0          | 266    | 9     | US-10-004-717-40   |
| 6          | 35    | 70.0          | 448    | 9     | US-09-738-626-6795 |
| 7          | 35    | 70.0          | 576    | 10    | US-09-925-297-787  |
| 8          | 34    | 68.0          | 251    | 9     | US-09-992-598-6    |
| 9          | 34    | 68.0          | 251    | 9     | US-09-989-293A-6   |
| 10         | 34    | 68.0          | 251    | 9     | US-09-989-735-6    |
| 11         | 34    | 68.0          | 251    | 9     | US-09-990-444-6    |
| 12         | 34    | 68.0          | 251    | 9     | US-09-989-730-6    |
| 13         | 34    | 68.0          | 251    | 9     | US-09-990-436-6    |
| 14         | 34    | 68.0          | 251    | 9     | US-09-991-181-6    |
| 15         | 34    | 68.0          | 251    | 9     | US-09-993-687-6    |
| 16         | 34    | 68.0          | 251    | 9     | US-09-989-734-6    |
| 17         | 34    | 68.0          | 251    | 9     | US-09-997-653-6    |
| 18         | 34    | 68.0          | 251    | 9     | US-10-174-590-2    |
| 19         | 34    | 68.0          | 251    | 9     | US-10-176-758-2    |

|    |    |      |     |   |                 |                   |
|----|----|------|-----|---|-----------------|-------------------|
| 20 | 34 | 68.0 | 251 | 9 | US-10-175-737-2 | Sequence 2, Appli |
| 21 | 34 | 68.0 | 251 | 9 | US-09-993-667-6 | Sequence 6, Appli |
| 22 | 34 | 68.0 | 251 | 9 | US-10-173-706-2 | Sequence 2, Appli |
| 23 | 34 | 68.0 | 251 | 9 | US-10-175-738-2 | Sequence 2, Appli |
| 24 | 34 | 68.0 | 251 | 9 | US-10-175-752-2 | Sequence 2, Appli |
| 25 | 34 | 68.0 | 251 | 9 | US-10-176-482-2 | Sequence 2, Appli |
| 26 | 34 | 68.0 | 251 | 9 | US-10-176-913-2 | Sequence 2, Appli |
| 27 | 34 | 68.0 | 251 | 9 | US-10-176-913-2 | Sequence 2, Appli |
| 28 | 34 | 68.0 | 251 | 9 | US-10-180-552-2 | Sequence 2, Appli |
| 29 | 34 | 68.0 | 251 | 9 | US-10-180-557-2 | Sequence 2, Appli |
| 30 | 34 | 68.0 | 251 | 9 | US-09-990-438-6 | Sequence 6, Appli |
| 31 | 34 | 68.0 | 251 | 9 | US-09-990-562-6 | Sequence 6, Appli |
| 32 | 34 | 68.0 | 251 | 9 | US-09-997-428-6 | Sequence 6, Appli |
| 33 | 34 | 68.0 | 251 | 9 | US-09-997-666-6 | Sequence 6, Appli |
| 34 | 34 | 68.0 | 251 | 9 | US-10-173-700-2 | Sequence 2, Appli |
| 35 | 34 | 68.0 | 251 | 9 | US-10-174-572-2 | Sequence 2, Appli |
| 36 | 34 | 68.0 | 251 | 9 | US-10-174-579-2 | Sequence 2, Appli |
| 37 | 34 | 68.0 | 251 | 9 | US-10-174-582-2 | Sequence 2, Appli |
| 38 | 34 | 68.0 | 251 | 9 | US-10-174-588-2 | Sequence 2, Appli |
| 39 | 34 | 68.0 | 251 | 9 | US-10-175-739-2 | Sequence 2, Appli |
| 40 | 34 | 68.0 | 251 | 9 | US-10-175-740-2 | Sequence 2, Appli |
| 41 | 34 | 68.0 | 251 | 9 | US-10-175-743-2 | Sequence 2, Appli |
| 42 | 34 | 68.0 | 251 | 9 | US-10-176-488-2 | Sequence 2, Appli |
| 43 | 34 | 68.0 | 251 | 9 | US-10-176-492-2 | Sequence 2, Appli |
| 44 | 34 | 68.0 | 251 | 9 | US-10-176-747-2 | Sequence 2, Appli |
| 45 | 34 | 68.0 | 251 | 9 | US-10-176-750-2 | Sequence 2, Appli |

#### ALIGNMENTS

RESULT 1  
US-09-839-447A-36  
; Sequence 36, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Salberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE REFERENCE: TRIPEP.020CPI  
; CURRENT APPLICATION NUMBER: US/09/839,447A  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-09-839-447A-36

Query Match 88.0% Score 44; DB 10; Length 20;  
Best Local Similarity 88.9%; Pred. No. 0.096;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
|||  
Db 7 RGTGTGFAY 15

RESULT 2  
US-09-839-447A-3  
; Sequence 3, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Salberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; FILE REFERENCE: TRIPEP.020CPI  
; CURRENT APPLICATION NUMBER: US/09/839,447A

; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-09-839-447A-3

Query Match 88.0%; Score 44; DB 10; Length 130;  
Best Local Similarity 88.9%; Pred. No. 0.58;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGCTGTGAY 9  
Db 97 RGCTGTGAY 105

## RESULT 3

US-10-105-929-15  
; Sequence 15, Application US/10105929  
; Patent No. US20020137142A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
; FILE REFERENCE: 09404/041001  
; CURRENT APPLICATION NUMBER: US/10/105,929  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,491  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058,108  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054,961  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-929-15

Query Match 74.0%; Score 37; DB 12; Length 247;  
Best Local Similarity 87.5%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTGAY 9  
Db 205 GTGTGTGAY 212

## RESULT 4

US-09-759-130B-137  
; Sequence 137, Application US/09759130B  
; Publication No. US20030022279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A.  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirst, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; FILE REFERENCE: MPI00-5350NMIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: US 09/608,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 137  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-759-130B-137

Query Match 74.0%; Score 37; DB 9; Length 248;  
Best Local Similarity 87.5%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGTGAY 9  
Db 205 GTGTGTGAY 212

## RESULT 5

US-10-004-717-40  
; Sequence 40, Application US/10004717  
; Publication No. US20020192665A1  
; GENERAL INFORMATION:  
; APPLICANT: ZOGHBI, HUDA Y.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN  
; TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS  
; TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION  
; FILE REFERENCE: P01899US4  
; CURRENT APPLICATION NUMBER: US/10/004,717  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 09/585,645  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: 60/176,993  
; PRIOR FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: 60/137,060  
; PRIOR FILING DATE: 1999-06-01  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Zebra Fish  
US-10-004-717-40

Query Match 74.0%; Score 37; DB 9; Length 266;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
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Db 209 RGTGVGYPY 217

## RESULT 6

US-09-738-626-6795  
; Sequence 6795, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TAKEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: Patentin ver. 3.0  
; SEQ ID NO 6795  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-6795

Query Match 70.0%; Score 35; DB 9; Length 448;  
Best Local Similarity 87.5%; Pred. No. 63;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFA 8  
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Db 386 RGTGTGAA 393

## RESULT 7

US-09-925-297-787  
; Sequence 787, Application US/09925297  
; Patent No. US20020081659A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA105  
; CURRENT APPLICATION NUMBER: US/09/925,297  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05989  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 928  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 787  
; LENGTH: 576  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-297-787

Query Match 70.0%; Score 35; DB 10; Length 576;  
Best Local Similarity 66.7%; Pred. No. 80;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
||||| :  
Db 499 RGHGTGFCF 507

## RESULT 8

US-09-992-598-6  
; Sequence 6, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 68.0%; Score 34; DB 9; Length 251;  
 Best Local Similarity 75.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9  
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 Db 65 GPGTGFLY 72

RESULT 9



US-09-989-293A-6  
Sequence 6, Application US/0989293A  
Patent No. US2002017164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P27301C66  
CURRENT APPLICATION NUMBER: US/09/989, 293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-12  
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PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
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RESULT 10  
US-09-989-735-6  
; Sequence 6, Application US/09099735  
; Publication No. US20020193299A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David

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;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC61  
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 ; Publication No. US20020193300A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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RESULT 12  
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Publication No. US2002019767A1  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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APPLICANT: Zhang, Zemin  
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CURRENT APPLICATION NUMBER: US/09/989,730  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
Db 65 GGTGFLY 72

RESULT 13  
US-09-990-436-6  
; Sequence 6, Application US/09990436  
; Publication No. US20020198148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730P1C14  
;; CURRENT APPLICATION NUMBER: US/09/990,436  
;; CURRENT FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
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Db 65 GPGTGFY 72

## RESULT 14

US-09-991-181-6  
; Sequence 6, Application US/09991181  
; Publication No. US20020197615A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
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; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2/30PIC53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; CURRENT FILING DATE: 2001-11-16  
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; PRIOR FILING DATE: 1997-06-16

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Fri Feb 14 15:00:53 2003

; PRIOR FILING DATE: 1998-06-16  
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; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFPAY 9  
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Db 65 GPGTGFY 72

RESULT 15

US-09-993-687-6  
; Sequence 6, Application US/09933687  
; Publication No. US20020198149A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C11  
; CURRENT APPLICATION NUMBER: US/09/993,687  
; CURRENT FILING DATE: 2002-11-14  
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| ; | PRIOR APPLICATION NUMBER: 60/090246 |
| ; | PRIOR FILING DATE: 1998-06-22       |
| ; | PRIOR APPLICATION NUMBER: 60/090252 |
| ; | PRIOR FILING DATE: 1998-06-22       |
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| ; | PRIOR FILING DATE: 1998-06-22       |
| ; | PRIOR APPLICATION NUMBER: 60/090349 |
| ; | PRIOR FILING DATE: 1998-06-23       |
| ; | PRIOR APPLICATION NUMBER: 60/090355 |
| ; | PRIOR FILING DATE: 1998-06-23       |
| ; | PRIOR APPLICATION NUMBER: 60/090429 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090431 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090435 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090444 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090445 |
| ; | PRIOR FILING DATE: 1998-06-24       |
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| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090535 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090540 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090542 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090557 |
| ; | PRIOR FILING DATE: 1998-06-24       |
| ; | PRIOR APPLICATION NUMBER: 60/090676 |
| ; | PRIOR FILING DATE: 1998-06-25       |
| ; | PRIOR APPLICATION NUMBER: 60/090678 |
| ; | PRIOR FILING DATE: 1998-06-25       |
| ; | PRIOR APPLICATION NUMBER: 60/090690 |
| ; | PRIOR FILING DATE: 1998-06-25       |
| ; | PRIOR APPLICATION NUMBER: 60/090694 |
| ; | PRIOR FILING DATE: 1998-06-25       |
| ; | PRIOR APPLICATION NUMBER: 60/090695 |
| ; | PRIOR FILING DATE: 1998-06-25       |
| ; | PRIOR APPLICATION NUMBER: 60/090696 |
| ; | PRIOR FILING DATE: 1998-06-25       |
| ; | PRIOR APPLICATION NUMBER: 60/090862 |
| ; | PRIOR FILING DATE: 1998-06-26       |
| ; | PRIOR APPLICATION NUMBER: 60/090863 |
| ; | PRIOR FILING DATE: 1998-06-26       |
| ; | PRIOR APPLICATION NUMBER: 60/091360 |
| ; | PRIOR FILING DATE: 1998-07-01       |
| ; | PRIOR APPLICATION NUMBER: 60/091478 |
| ; | PRIOR FILING DATE: 1998-07-02       |
| ; | PRIOR APPLICATION NUMBER: 60/091544 |

; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 68.0%; Score 34; DB 9; Length 251;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OV 2 GTGTGFAY 9  
| | | | |  
65 GPGTGFLY 72

Search completed: February 14, 2003, 11:21:30  
Job time : 6.22581 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 9 Seconds  
(without alignments)  
96.134 Million cell updates/sec

Title: US-09-701-001B-3

Perfect score: 50

Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 39    | 78.0        | 685    | 2 A83499 | probable lipoxigen |
| 2          | 38    | 76.0        | 483    | 2 E84976 | tlld protein [impo |
| 3          | 38    | 76.0        | 568    | 2 A45804 | Ig mu chain C regi |
| 4          | 37    | 74.0        | 280    | 2 A39484 | androgen-withdraw  |
| 5          | 37    | 74.0        | 502    | 2 AE2040 | hypothetical prote |
| 6          | 36    | 72.0        | 101    | 2 T10856 | carboxypeptidase C |
| 7          | 36    | 72.0        | 149    | 2 S19130 | rab15 protein - wh |
| 8          | 36    | 72.0        | 163    | 2 S01152 | RAB21 protein - ri |
| 9          | 36    | 72.0        | 165    | 2 T03392 | probable dehydrin  |
| 10         | 36    | 72.0        | 411    | 1 A35275 | carboxypeptidase C |
| 11         | 36    | 72.0        | 423    | 1 A33383 | probable MFS trans |
| 12         | 36    | 72.0        | 429    | 1 T03607 | probable carboxype |
| 13         | 36    | 72.0        | 498    | 1 A29412 | carboxypeptidase C |
| 14         | 36    | 72.0        | 500    | 1 S22330 | carboxypeptidase C |
| 15         | 36    | 72.0        | 1077   | 2 H96007 | probable acriflavi |
| 16         | 36    | 72.0        | 3295   | 2 AE0074 | probable adhesin Y |
| 17         | 35    | 70.0        | 163    | 2 A89904 | conserved hypothet |
| 18         | 35    | 70.0        | 398    | 2 C95278 | hypothetical prote |
| 19         | 35    | 70.0        | 401    | 2 AD2451 | serine proteinase  |
| 20         | 35    | 70.0        | 429    | 2 AD1894 | serine proteinase  |
| 21         | 35    | 70.0        | 452    | 2 S77538 | TRBP151 - human    |
| 22         | 35    | 70.0        | 563    | 2 G02043 | period clock prote |
| 23         | 35    | 70.0        | 713    | 1 UMMS   | outer layer protei |
| 24         | 35    | 70.0        | 736    | 1 VPXRPC | outer capsid spike |
| 25         | 35    | 70.0        | 744    | 2 S45060 | outer capsid spike |
| 26         | 35    | 70.0        | 744    | 2 S45061 | villin - chicken   |
| 27         | 35    | 70.0        | 826    | 1 A31822 | Ig heavy chain - c |
| 28         | 35    | 70.0        | 1005   | 2 T18537 | hypothetical prote |
| 29         | 34    | 68.0        | 99     | 2 F82709 |                    |

ALIGNMENTS

RESULT 1

A83499

Probable lipoxigenase Pali69 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: A83499  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A83499  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-685 <STO>  
A:Cross-references: GB:AE004547; GB:AE004091; MID:99947089; PIDN:AAG04558.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: Pali69

Query Match 78.0%; Score 39; DB 2; Length 685;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
| | | | | | | | | |  
Db 305 TGTGFAY 311

RESULT 2

E84976

tlld protein [imported] - Buchnera sp. (strain APS)  
C:Species: Buchnera sp.  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: E84976  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp  
A:Reference number: A84930; MUID:20445173; PMID:10993077  
A:Accession: E84976  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-483 <STO>  
A:Cross-references: GB:AF000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: tlld; BU398  
C:Superfamily: Escherichia coli tlld protein  
Query Match 76.0%; Score 38; DB 2; Length 483;  
Best Local Similarity 77.8%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCTGTGFAY 9  
||| |||||  
Db 72 RGESTGFAY 80

## RESULT 3

A45804  
Ig mu chain C region precursor, secreted form - channel catfish  
C:Species: Ictalurus punctatus (channel catfish)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jul-2000  
C:Accession: A45804; A30331; S12833  
R:Ghaffari, S.H.; Lobb, C.J.  
J. Immunol. 143, 2730-2739, 1989  
A:Title: Nucleotide sequence of channel catfish heavy chain cDNA and genomic blot analysis  
A:Reference number: A45804; MUID:90010149; PMID:2507636  
A:Accession: A45804  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-568 <GHA>  
A:Cross-references: GB:M27230; NID:g213318; PIDN:AAA79003.1; PID:g213319  
Ghaffari, S.H.; Lobb, C.J.  
J. Immunol. 142, 1356-1365, 1989  
A:Title: Cloning and sequence analysis of channel catfish heavy chain cDNA indicate phylogenetic relationship between channel catfish and rainbow trout  
A:Reference number: A30331; MUID:89124381; PMID:2492581  
A:Accession: A30331  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 325-568 <GH2>  
A:Cross-references: GB:M23733; NID:g213316; PIDN:AAA49329.1; PID:g213317  
R:Wilson, M.R.; Marcuz, A.; van Ginkel, F.; Miller, N.W.; Clem, L.W.; Middleton, D.; War  
Nucleic Acids Res. 18, 5227-5233, 1990  
A:Title: The immunoglobulin M heavy chain constant region gene of the channel catfish, Ictalurus punctatus  
A:Reference number: S12833; MUID:90384824; PMID:2119496  
A:Accession: S12833  
A:Molecule type: DNA  
A:Residues: 135-568 <WIL>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; heterotetramer; immunoglobulin  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-568/Product: Ig mu chain C region, secreted form #status predicted <MAT>  
F:31-113/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 38; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGTGFA 8  
|||||  
70 GTGTGFA 76

## RESULT 4

A39484  
androgen-withdrawal apoptosis protein RVP1, prostatic - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 04-Mar-2000  
C:Accession: A39484  
R:Briehl, M.M.; Miesfeld, R.L.  
Mol. Endocrinol. 5, 1381-1388, 1991  
A:Title: Isolation and characterization of transcripts induced by androgen withdrawal and androgen withdrawal  
A:Reference number: A39484; MUID:92130987; PMID:1723140  
A:Accession: A39484  
A:Molecule type: mRNA  
A:Residues: 1-280 <BRI>  
A:Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858  
C:Genetics:  
C:Superfamily: rat androgen-withdrawal apoptosis protein RVP1

Query Match 74.0%; Score 37; DB 2; Length 280;  
Best Local Similarity 87.5%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
|||||  
Db 205 GTGTGFAY 212

## RESULT 5

AE2040  
hypothetical protein all1875 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AE2040  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig  
Nakaazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE2040  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-502 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BAF73574.1; PID:g17130965; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1875

Query Match 74.0%; Score 37; DB 2; Length 502;  
Best Local Similarity 77.8%; Pred. No. 75;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
||:|||||  
Db 159 RGSCTGEAY 167

## RESULT 6

T10856  
carboxypeptidase C (EC 3.4.16.5) - mung bean (fragment)  
N:Alternate names: serine carboxypeptidase II  
C:Species: Vigna radiata (mung bean)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 08-Dec-2000  
C:Accession: T10856  
R:Lee, K.; Tan-Wilson, A.L.; Wilson, K.A.  
Submitted to the EMBL Data Library, February 1996  
A:Reference number: Z17185  
A:Accession: T10856  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-101 <LEE>  
A:Cross-references: EMBL:U49382; NID:g1223915; PID:g1223916  
A:Experimental source: strain Jumbo; tissue\_type cotyledons; clone pKL054  
C:Superfamily: serine carboxypeptidase  
C:Keywords: hydrolase; serine carboxypeptidase

Query Match 72.0%; Score 36; DB 2; Length 101;  
Best Local Similarity 85.7%; Pred. No. 24;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||  
Db 49 TGTGFSY 55

## RESULT 7

S19130  
rab15 protein - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Aug-1999  
C:Accession: S19130; S16758  
R:King, S.W.; Joshi, C.P.; Nguyen, H.T.  
Plant Mol. Biol. 18, 119-121, 1992

A:Title: DNA sequence of an ABA-responsive gene (rab 15) from water-stressed wheat roots

A:Reference number: S19130; MUID:92119217; PMID:1531029

A:Accession: S19130

A:Molecule type: mRNA

A:Residues: 1-149 <KIN>

A:Cross-references: EMBL:X59133; NID:g21850; PIDN:CAA41850.1; PID:g21851

C:Genetics:

A:Gene: rab15

C:Superfamily: dehydrin-like protein

Query Match 72.0%; Score 36; DB 2; Length 149;  
Best Local Similarity 87.5%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9

|||||

Db 99 GTGTGGAY 106

RESULT 8

S01152

C:Species: Oryza sativa (rice)

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1990 #text\_change 20-Aug-1999

C:Accession: S01152

R:Mundy, J.; Chua, N.H.

EMBO J. 7, 2279-2286, 1988

A:Title: Abscisic acid and water-stress induce the expression of a novel rice gene.

A:Reference number: S01152; MUID:89052639; PMID:2973410

A:Accession: S01152

A:Molecule type: DNA

A:Residues: 1-163 <MUN>

A:Cross-references: EMBL:X00842; NID:g20316; PIDN:CAA68765.1; PID:g295826

A:Note: the authors translated the codon GCG for residue 28 as Gly

C:Genetics:

A:Gene: RAB21

A:Introns: 70/3

C:Superfamily: dehydrin-like protein

C:Keywords: seed

Query Match 72.0%; Score 36; DB 2; Length 163;  
Best Local Similarity 87.5%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9

|||||

Db 114 GTGTGGAY 121

RESULT 9

T03392

C:Species: Oryza sativa (rice)

C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 20-Aug-1999

C:Accession: T03392

R:McEvoy, S.M.; Sheoran, I.S.; Saini, H.S.

submitted to the EMBL Data Library, June 1996

A:Description: A rice cDNA encoding a late embryogenesis abundant protein.

A:Reference number: Z14923

A:Accession: T03392

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-165 <MCE>

A:Cross-references: EMBL:U60097; NID:g1399912; PIDN:AAB03330.1; PID:g1399913

C:Superfamily: dehydrin-like protein

Query Match 72.0%; Score 36; DB 2; Length 165;  
Best Local Similarity 87.5%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGTGFAY 9

|||||

Db 116 GTGTGGAY 123

RESULT 10

A35275

C:Species: Oryza sativa (rice)

C:Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999

C:Accession: A35275

R:Sorensen, S.B.; Svendsen, I.; Breddam, K.

Carlsberg Res. Commun. 54, 193-202, 1989

A:Title: Primary structure of carboxypeptidase III from malted barley.

A:Reference number: A35275; MUID:90315015; PMID:2639682

A:Accession: A35275

A:Molecule type: protein

A:Residues: 1-411 <SOR>

A:Note: 185-Val was also found

C:Superfamily: serine carboxypeptidase

C:Keywords: blocked amino end; glycoprotein; hydrolase; serine carboxypeptidase

F:1/Modified site: blocked amino end (Leu) (probably acetylated) #status experimental

F:71/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:143,331,388/Active site: Ser, Asp, His #status predicted

Query Match 72.0%; Score 36; DB 1; Length 411;  
Best Local Similarity 85.7%; Pred. No. 92;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGTGFAY 9

|||||

Db 94 TGTGFSY 100

RESULT 11

A83383

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: A83383

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: A83383

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-423 <STO>

A:Cross-references: GB:AE004638; GB:AE004091; NID:g9948116; PIDN:AAG05502.1; GSPDB:G

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2114

C:Superfamily: Escherichia coli hypothetical protein b4279

Query Match 72.0%; Score 36; DB 2; Length 423;  
Best Local Similarity 66.7%; Pred. No. 94;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RGTGTGFAY 9

|||||

Db 360 RGSQGFY 368

RESULT 12

T03607

C:Species: Oryza sativa (rice)

C:Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 21-Jul-2000

C:Accession: T03607

R:Washio, K.; Ishikawa, K.

Plant Physiol. 105, 1275-1280, 1994

A:Title: Organ-specific and hormone-dependent expression of genes for serine carboxyp

A:Reference number: 214975; MUID:95062718; PMID:7972496  
A:Accession: T03607  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-429 <WAS>  
A:Cross-references: EMBL:D17587; NID:g409581; PIDN:BA04511.1; PID:g409582  
A:Experimental source: cv. Yukihiikari  
C:Genetics:

A:Gene: cbp31  
C:Superfamily: serine carboxypeptidase  
C:Keywords: glycoprotein; hydrolase; serine carboxypeptidase  
F:76,414,417/Binding site: carboxyl-terminal (Asn) (covalent) #status predicted  
F:148,336,393/Active site: Ser, Asp, His #status predicted

Query Match 72.0%; Score 36; DB 1; Length 429;  
Best Local Similarity 85.7%; Pred. No. 96;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||:|  
99 TGTGFSY 105

## RESULT 13

A:29412  
carboxypeptidase C (EC 3.4.16.5) precursor - wheat  
N:Alternate names: carboxypeptidase Y homolog  
C:Species: Triticum aestivum (common wheat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Nov-1999  
C:Accession: A29412  
R:Baulcombe, D.C.; Barker, R.F.; Jarvis, M.G.  
J. Biol. Chem. 262, 13726-13735, 1987  
A:Title: A gibberellin responsive wheat gene has homology to yeast carboxypeptidase Y.  
A:Reference number: A29412; MUID:88007602; PMID:2820978  
A:Accession: A29412  
A:Molecule type: mRNA  
A:Residues: 1-499 <BAU>  
C:Genetics:

A:Introns: 100/2; 156/3; 196/3; 244/3; 295/1; 324/3; 411/1; 455/3

C:Superfamily: serine carboxypeptidase  
C:Keywords: glycoprotein; hydrolase; serine carboxypeptidase; zymogen  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-73/Domain: propeptide #status predicted <PRO>  
F:74-484/Product: carboxypeptidase C #status predicted <MAT>  
F:485-499/Domain: carboxyl-terminal propeptide #status predicted <CPRO>  
F:144/Binding site: carboxyl-terminal (Asn) (covalent) #status predicted  
F:216,404,461/Active site: Ser, Asp, His #status predicted

Query Match 72.0%; Score 36; DB 1; Length 499;  
Best Local Similarity 85.7%; Pred. No. 1.le+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||:|  
Db 167 TGTGFSY 173

## RESULT 14

A:S22530  
carboxypeptidase C (EC 3.4.16.5) precursor - rice  
N:Alternate names: carboxypeptidase III  
C:Species: Oryza sativa (rice)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Nov-1999  
C:Accession: S22530  
R:Washio, K.; Ishikawa, K.  
Plant Mol. Biol. 19, 631-640, 1992  
A:Title: Structure and expression during the germination of rice seeds of the gene for a  
A:Reference number: S22530; MUID:92329723; PMID:1627776  
A:Accession: S22530  
A:Molecule type: DNA  
A:Residues: 1-500 <WAS>  
A:Cross-references: EMBL:S40458  
C:Genetics:

A:Introns: 100/2; 156/3; 196/3; 244/3; 285/1; 324/3; 411/1; 455/3  
C:Superfamily: serine carboxypeptidase  
C:Keywords: glycoprotein; hydrolase; serine carboxypeptidase; zymogen  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-73/Domain: propeptide #status predicted <PRO>  
F:74-484/Product: carboxypeptidase C #status predicted <MAT>  
F:485-499/Domain: carboxyl-terminal propeptide #status predicted <CPRO>  
F:144/Binding site: carboxyl-terminal (Asn) (covalent) #status predicted  
F:216,404,461/Active site: Ser, Asp, His #status predicted

Query Match 72.0%; Score 36; DB 1; Length 500;  
Best Local Similarity 85.7%; Pred. No. 1.le+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||:|  
Db 167 TGTGFSY 173

## RESULT 15

A:H96007  
probable acriflavin resistance protein [imported] - Sinorhizobium meliloti (strain 10  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: H96007  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,883-Kb pSymb megaplasmid from the N2-fixing e  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: H96007  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1077 <KUR>  
A:Cross-references: GB:AL591985; PIDN:CAC49728.1; PID:gl5141215; GSPDB:GN00167  
A:Experimental source: strain 1021, megaplasmid pSymb  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau  
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wellis, D.H.; Wong, K.; Yeh,  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
C:Genetics:

A:Contents: annotation

C:Genetics:

A:Gene: acrF: Smb21498

A:Genome: plasmid

C:Superfamily: acriflavin resistance protein

Query Match 72.0%; Score 36; DB 2; Length 1077;  
Best Local Similarity 75.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
|||||:|  
Db 673 GTGGGFAY 680

Search completed: February 14, 2003, 11:19:46  
Job time : 11 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 4.64516 Seconds  
(without alignments)  
80.360 Million cell updates/sec

Title: US-09-701-001b-3  
Perfect score: 50  
Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Hit: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID        | Description         |
|------------|-------|---------------|--------|--------------|---------------------|
| 1          | 38    | 76.0          | 483    | 1 TLDD_BUCAI | P57478 buchnera ap  |
| 2          | 37    | 74.0          | 219    | 1 CLD3_MOUSE | Q92099 mus musculus |
| 3          | 37    | 74.0          | 219    | 1 CLD3_RAT   | Q63400 rattus norv  |
| 4          | 36    | 72.0          | 149    | 1 DH15_WHEAT | Q00742 triticum ae  |
| 5          | 36    | 72.0          | 163    | 1 DH21_ORYSA | P12253 oryza sativ  |
| 6          | 36    | 72.0          | 429    | 1 CBPX_ORYSA | P52712 oryza sativ  |
| 7          | 36    | 72.0          | 500    | 1 CBP3_ORYSA | P37891 oryza sativ  |
| 8          | 36    | 72.0          | 500    | 1 CBP3_WHEAT | P11515 triticum ae  |
| 9          | 36    | 72.0          | 508    | 1 CBP3_HORVU | P21529 hordeum vul  |
| 10         | 35    | 70.0          | 672    | 1 PHX5_MOUSE | P08399 mus musculus |
| 11         | 35    | 70.0          | 736    | 1 VP4_ROTPE  | P26193 porcine rot  |
| 12         | 35    | 70.0          | 826    | 1 VILI_CHICK | P02640 gallus gall  |
| 13         | 34    | 68.0          | 111    | 1 CYC_CHLRE  | P15451 chlanydomon  |
| 14         | 34    | 68.0          | 233    | 1 YOD2_CAEEL | P34594 caenorhabdi  |
| 15         | 34    | 68.0          | 291    | 1 CCAS_CHICK | Q42398 gallus gall  |
| 16         | 34    | 68.0          | 281    | 1 SUHB_MYCLE | P46813 mycobacteri  |
| 17         | 34    | 68.0          | 369    | 1 H181_STRCO | P16246 streptomyce  |
| 18         | 34    | 68.0          | 375    | 1 Y4ED_RHISN | P55427 rhizobium s  |
| 19         | 34    | 68.0          | 450    | 1 TBA2_HUMAN | Q13748 homo sapien  |
| 20         | 34    | 68.0          | 450    | 1 TBA3_MOUSE | P05214 mus musculus |
| 21         | 34    | 68.0          | 450    | 1 TBA2_ONCMY | P18288 oncorhynch   |
| 22         | 34    | 68.0          | 451    | 1 TBA2_HOMAN | Q94570 homarus ame  |
| 23         | 34    | 68.0          | 477    | 1 GLGA_STRPN | Q97qs5 streptococ   |
| 24         | 34    | 68.0          | 640    | 1 Y0AA_HAEIN | P44680 haemophilus  |
| 25         | 34    | 68.0          | 905    | 1 CTFE_MYCTU | Q10860 mycobacteri  |
| 26         | 34    | 68.0          | 1394   | 1 HAP_HAEIN  | P45387 haemophilus  |
| 27         | 34    | 68.0          | 1401   | 1 RPOC_VIBCH | Q9kv29 vibrio chol  |
| 28         | 34    | 68.0          | 1415   | 1 RPOC_HAEIN | P43739 haemophilus  |
| 29         | 33    | 66.0          | 157    | 1 Y188_RICPR | Q9zdx6 rickettsia   |
| 30         | 33    | 66.0          | 356    | 1 PROB_AQUAE | O67209 aquifex aeo  |
| 31         | 33    | 66.0          | 385    | 1 ARGD_AQUAE | P36839 bacillus su  |
| 32         | 33    | 66.0          | 405    | 1 YJHB_ECOLI | P39352 escherichia  |
| 33         | 33    | 66.0          | 445    | 1 ALCP_BACP3 | P30145 bacillus ps  |

|    |    |      |     |              |                    |
|----|----|------|-----|--------------|--------------------|
| 34 | 33 | 66.0 | 561 | 1 HEMA_IACKG | P12581 influenza a |
| 35 | 33 | 66.0 | 637 | 1 DXS_NEIMA  | Q9jw13 neisseria m |
| 36 | 33 | 66.0 | 637 | 1 DXS_NEIMB  | Q9jxv7 neisseria m |
| 37 | 33 | 66.0 | 887 | 1 SM6B_RAT   | O70141 rattus norv |
| 38 | 33 | 66.0 | 893 | 1 DSCI_BOVIN | Q01107 bos taurus  |
| 39 | 33 | 66.0 | 984 | 1 KBFL_CHICK | Q04861 gallus gall |
| 40 | 32 | 64.0 | 204 | 1 RL15_ORCLI | Q9xyc2 orconectes  |
| 41 | 32 | 64.0 | 309 | 1 ALSK_ECOLI | P32718 escherichia |
| 42 | 32 | 64.0 | 321 | 1 HHOA_ARATH | O9sel7 arabidopsis |
| 43 | 32 | 64.0 | 338 | 1 GALE_PASHA | O59678 pasteurella |
| 44 | 32 | 64.0 | 339 | 1 GALE_BACSU | P55180 bacillus su |
| 45 | 32 | 64.0 | 347 | 1 GALE_RAT   | P18645 rattus norv |

## ALIGNMENTS

| RESULT 1 | TLDD_BUCAI   | STANDARD; | PRT; | 483 AA. |
|----------|--|-----------|------|---------|
| AC       | P57478;  |           |      |         |
| DT       | 16-OCT-2001 (Rel. 40, Created)   |           |      |         |
| DT       | 16-OCT-2001 (Rel. 40, Last sequence update)                                |           |      |         |
| DE       | 16-OCT-2001 (Rel. 40, Last annotation update)                              |           |      |         |
| DE       | TlDD protein homolog.  |           |      |         |
| GN       | TLDD OR BU398.   |           |      |         |
| OS       | Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum)     |           |      |         |
| OS       | symbiotic bacterium).  |           |      |         |
| OX       | Bacteria; Proteobacteria; gamma subdivision; Buchnera.                     |           |      |         |
| OX       | NCBI_TaxID=118099;   |           |      |         |
| RN       | [1]  |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |      |         |
| RC       | STRAIN-Tokyo. 1998;  |           |      |         |
| RX       | MEDLINE=20445173; PubMed=10993077;   |           |      |         |
| RA       | Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;             |           |      |         |
| RT       | "Genome sequence of the endocellular bacterial symbiont of aphids          |           |      |         |
| RT       | Buchnera sp. APS."   |           |      |         |
| RL       | Nature 407:81-86(2000).  |           |      |         |
| CC       | -1- SIMILARITY: BELONGS TO THE TLDD/PMBA FAMILY.                           |           |      |         |
| CC       | -----  |           |      |         |
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| CC       | modified and this statement is not removed. Usage by and for commercial    |           |      |         |
| CC       | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |           |      |         |
| CC       | or send an email to license@isb-sib.ch).                                   |           |      |         |
| CC       | -----  |           |      |         |
| DR       | EMBL; AP001119; BABI3101.1; -  |           |      |         |
| DR       | InterPro; IPR002510; PmbA_TlDD.  |           |      |         |
| DR       | Pfam; PF01523; PmbA_TlDD; 1.   |           |      |         |
| KW       | Complete proteome.   |           |      |         |
| SQ       | SEQUENCE 483 AA; 52977 MW; A05CE98518720EBA CRC64;                         |           |      |         |

Query Match 76.0%; Score 38; DB 1; Length 483;  
Best Local Similarity 77.8%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
|||  
Db 72 RGTGTGFAY 80

## RESULT 2

| CLD3_MOUSE | STANDARD;  | PRT; | 219 AA. |
|------------|--|------|---------|
| ID         | CLD3_MOUSE   |      |         |
| AC         | Q920G9; Q91X40;  |      |         |
| DT         | 30-MAY-2000 (Rel. 39, Created)                                   |      |         |
| DT         | 30-MAY-2000 (Rel. 39, Last sequence update)                      |      |         |
| DT         | 15-JUN-2002 (Rel. 41, Last annotation update)                    |      |         |
| DE         | Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE- |      |         |
| DE         | receptor 2) (CPE-R 2).   |      |         |
| GN         | CLDN3 OR CPETR2.   |      |         |

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=99097345; PubMed=9878248;  
 RA Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.;  
 RT "Genes for the CPE receptor (CPETR1) and the human homolog of RVPL  
 RT (CPETR2) are localized within the Williams-Beuren syndrome deletion.";  
 RL Genomics 54:453-459(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=99110921; PubMed=9892664;  
 RA Morita K., Furuse M., Fujimoto K., Tsukita S.;  
 RT "Claudin multigene family encoding four-transmembrane domain protein  
 RT components of tight junction strands.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX TISSUE=Colon;  
 RA Strausberg R.;  
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be  
 CC produced by alternative splicing.  
 CC -!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF095905; AAD14608.1; -;  
 DR EMBL; AF095905; AAD14608.1; -;  
 DR EMBL; AF097821; AAD09756.1; -;  
 DR EMBL; BC012650; AAH12650.1; -;  
 DR MGI; MGI:1329044; Clgdn3.  
 DR InterPro; IPR001832; Claudin.  
 DR Pfam; PF00822; PMP22\_Claudin; 1.  
 DR PRINTS; PR01077; CLAUDIN.  
 DR PROSITE; PS01346; CLAUDIN; 1.  
 DR TIGHT junction; Transmembrane; Alternative splicing.  
 DR TRANSMEM 9 29 POTENTIAL.  
 FT TRANSMEM 81 101 POTENTIAL.  
 FT TRANSMEM 116 136 POTENTIAL.  
 FT TRANSMEM 160 180 POTENTIAL.  
 FT TRANSMEM 180 180 POTENTIAL.  
 FT VARSPLIC 72 91 MISSING (IN ISOFORM 2).  
 FT SEQUENCE 219 AA; 23284 MW; 62F67810D9B9BD37 CRC64;  
 SQ  
 Query Match 74.0%; Score 37; DB 1; Length 219;  
 Best Local Similarity 87.5%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GTGTGFAY 9  
 |||||  
 Db 206 GTGTGTAY 213  
 RESULT 3  
 CLD3\_RAT  
 ID CLD3\_RAT STANDARD; PRT; 219 AA.  
 AC Q63400;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Claudin-3 (Ventral prostate.1 protein) (RVPL).  
 GN CLDN3.  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92130987; PubMed=1723140;  
 RA Brichl M.M., Miesfeld R.L.;  
 RT "Isolation and characterization of transcripts induced by androgen  
 RT withdrawal and apoptotic cell death in the rat ventral prostate.";  
 RL Mol. Endocrinol. 5:1381-1388(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Keen T.J., Inglehearn C.F.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M74067; AAA41760.1; -;  
 DR EMBL; AJ011656; CAA09727.1; -;  
 DR InterPro; IPR001832; Claudin.  
 DR Pfam; PF00822; PMP22\_Claudin; 1.  
 DR PRINTS; PR01077; CLAUDIN.  
 DR PROSITE; PS01346; CLAUDIN; 1.  
 DR TIGHT junction; Transmembrane.  
 DR TRANSMEM 9 29 POTENTIAL.  
 FT TRANSMEM 81 101 POTENTIAL.  
 FT TRANSMEM 116 136 POTENTIAL.  
 FT TRANSMEM 162 182 POTENTIAL.  
 FT CONFLICT 4 4 G -> S (IN REF. 1).  
 FT CONFLICT 55 55 MISSING (IN REF. 1).  
 FT CONFLICT 217 219 DIV -> YTSRPGARTPHHHYQPSMYTRPACSLASETT  
 PPSRRLOTPRSLLARLEDRQGVFPSPVAT (IN REF. 1).  
 SQ SEQUENCE 219 AA; 23314 MW; 820CC6BFC20D122D CRC64;  
 Query Match 74.0%; Score 37; DB 1; Length 219;  
 Best Local Similarity 87.5%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GTGTGFAY 9  
 |||||  
 Db 206 GTGTGTAY 213  
 RESULT 4  
 DH15\_WHEAT  
 ID DH15\_WHEAT STANDARD; PRT; 149 AA.  
 AC Q00742;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE Dehydrin RAB 15.  
 GN RAB 15.  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CV. TAM W-101; TISSUE=Root;  
 RX MEDLINE=92119217; PubMed=1531029;  
 RA King S.W., Joshi C.P., Nguyen H.T.;

"DNA sequence of an ABA-responsive gene (rab 15) from water-stressed wheat roots.";  
 Plant Mol. Biol. 18:119-121(1992).  
 CC -!- INDUCTION: BY ABSCISIC ACID AND WATER STRESS.  
 CC -!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X59133; CAA41850.1; -.  
 DR PIR; S16758; S16758.  
 DR PIR; S19130; S19130.  
 DR InterPro; IPR000167; Dehydrin.  
 DR Pfam; PF00257; dehydrin; 1.  
 DR PROSITE; PS00315; DEHYDRIN\_1; 1.  
 DR PROSITE; PS00823; DEHYDRIN\_2; 2.  
 DR DOMAIN 55 64 POLY-SER.  
 DR DEHYDRIN.  
 KW Dehydrin.  
 FT DOMAIN 55 64 POLY-SER.  
 FT SEQUENCE 149 AA; 15766 MW; 72183F7A99E467B1 CRC64;  
 SQ SEQUENCE 149 AA; 15766 MW; 72183F7A99E467B1 CRC64;  
 Query Match 72.0%; Score 36; DB 1; Length 149;  
 Best Local Similarity 87.5%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GTGTGGFAY 9  
 DB 99 GTGTGGAY 106  
 RESULT 5  
 ID DH21-ORYSA STANDARD; PRT; 163 AA.  
 AC P12253;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Water-stress inducible protein RAB21.  
 GN RAB21.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Indica-IR36; TISSUE=Seed;  
 RA MEDLINE=89052639; PubMed=2973410;  
 RA Mundy J.W., Chua N.-H.;  
 RT "Abscisic acid and water-stress induce the expression of a novel rice  
 gene.";  
 RL EMBO J. 7:2279-2286(1988).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: BY ABSCISIC ACID (ABA) AND WATER STRESS.  
 CC -!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.  
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 CC -----  
 DR EMBL; Y00842; CAA68765.1; -.  
 DR PIR; S01152; S01152.  
 DR InterPro; IPR000167; Dehydrin.  
 DR Pfam; PF00257; dehydrin; 1.  
 DR PROSITE; PS00315; DEHYDRIN\_1; 1.

DR PROSITE; PS00823; DEHYDRIN\_2; 2.  
 KW Dehydrin; Seed: Seed embryo; Repeat.  
 FT DOMAIN 63 71 TYPE A.  
 FT REPEAT 3 28 TYPE A.  
 FT REPEAT 79 96 TYPE B.  
 FT REPEAT 114 140 TYPE A.  
 FT REPEAT 147 163 TYPE B.  
 SQ SEQUENCE 163 AA; 16543 MW; 47FEDAD256DE7ACF CRC64;  
 Query Match 72.0%; Score 36; DB 1; Length 163;  
 Best Local Similarity 87.5%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GTGTGGFAY 9  
 DB 114 GTGTGGAY 121  
 RESULT 6  
 ID CBPX-ORYSA STANDARD; PRT; 429 AA.  
 AC P52712;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine carboxypeptidase-like precursor (EC 3.4.16.-).  
 GN CBP31.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Yukihikari;  
 RA Washio K., Ishikawa K.;  
 RA Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.  
 RL -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a  
 CC broad specificity.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.  
 CC -----  
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 CC -----  
 DR EMBL; D17587; BAA04511.1; -.  
 DR HSP; P00729; IYSC.  
 DR MEROPS; S10.009; -.  
 DR InterPro; IPR000379; Ser\_estrs\_site.  
 DR InterPro; IPR001563; Serine\_carbpept.  
 DR Pfam; PF00450; serine\_carbpept; 1.  
 DR PRINTS; PR00724; CRBOXYPTASEC.  
 DR PRODOM; PD001189; Serine\_carbpept; 1.  
 DR PROSITE; PS00131; CARBOXYPEPT\_SER\_SER; 1.  
 DR PROSITE; PS00560; CARBOXYPEPT\_SER\_HIS; 1.  
 KW Hydrolase; Carboxypeptidase; Glycoprotein; Signal.  
 FT SIGNAL 1 ? POTENTIAL.  
 FT CHAIN 1 429 SERINE CARBOXYPEPTIDASE-LIKE.  
 FT ACT\_SITE 148 148 BY SIMILARITY.  
 FT ACT\_SITE 336 336 BY SIMILARITY.  
 FT ACT\_SITE 393 393 BY SIMILARITY.  
 FT BINDING 339 339 SUBSTRATE (BY SIMILARITY).  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 429 AA; 47746 MW; 1D9A668544325BB1 CRC64;  
 Query Match 72.0%; Score 36; DB 1; Length 429;  
 Best Local Similarity 85.7%; Pred. No. 48;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||:|

Db 99 TGTGFSY 105

RESULT 7  
CBP3\_ORYSA  
ID CBP3\_ORYSA STANDARD; PRT; 500 AA.  
AC P37891;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serine carboxypeptidase III precursor (EC 3.4.16.5).  
GN CBP3.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
NCBI\_TaxID=4530;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=cv. Yukihikari; TISSUE=Seed;  
RX MEDLINE=92329723; PubMed=1627776;  
RA Washio K., Ishikawa K.;  
RT "Structure and expression during the germination of rice seeds of the  
RT gene for a carboxypeptidase.";  
RL Plant Mol. Biol. 19:631-640(1992).  
CC -1- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a  
CC broad specificity.  
CC -1- SUBUNIT: MONOMER (PROBABLE).  
CC -1- INDUCTION: BY GIBBERELIC ACID (GA). INHIBITED BY ABSCISIC ACID  
CC (ABA).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D10985; BAA01757.1; -.  
CC PIR; S22530; S22530.  
CC HSSP; P00729; LYSC.  
CC MEROPS; S10.009; -.  
CC InterPro; IPR000379; Ser\_estrs.site.  
CC Pfam; PF00450; serine\_carbpept.  
CC PRINTS; PR00724; CRBOXYPTASEC.  
CC ProDom; PD001189; Serine\_carbpept; 1.  
CC PROSITE; PS00131; CARBOXYPEPT\_SER\_SER; 1.  
CC PROSITE; PS00560; CARBOXYPEPT\_SER\_HIS; 1.  
CC Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT PROPEP 22 73 BY SIMILARITY.  
FT CHAIN 74 484 SERINE CARBOXYPEPTIDASE III.  
FT PROPEP 485 500 BY SIMILARITY.  
FT ACT\_SITE 216 216 BY SIMILARITY.  
FT ACT\_SITE 404 404 BY SIMILARITY.  
FT ACT\_SITE 461 461 BY SIMILARITY.  
FT BINDING 407 407 SUBSTRATE (BY SIMILARITY).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 500 AA; 55446 MW; AE455E2780147DB8 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 500;  
Best Local Similarity 85.7%; Pred. No. 56;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||:|

Db 167 TGTGFSY 173

RESULT 8  
CBP3\_WHEAT  
ID CBP3\_WHEAT STANDARD; PRT; 500 AA.  
AC P11515;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serine carboxypeptidase III precursor (EC 3.4.16.5) (CP-WIII).  
GN CBP3.  
OS Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Triticum.  
NCBI\_TaxID=4565;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=88007602; PubMed=2820978;  
RA Baulcombe D.C., Barker R.F., Jarvis M.G.;  
RT "A gibberellin responsive wheat gene has homology to yeast  
RT carboxypeptidase Y.";  
RL J. Biol. Chem. 262:13726-13735(1987).  
CC -1- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a  
CC broad specificity.  
CC -1- SUBUNIT: MONOMER (PROBABLE).  
CC -1- INDUCTION: BY GIBBERELIC ACID (GA).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; J02817; AAA34273.1; -.  
CC PIR; A29412; A29412.  
CC HSSP; P00729; 1CYP.  
CC MEROPS; S10.009; -.  
CC InterPro; IPR000379; Ser\_estrs.site.  
CC Pfam; PF00450; serine\_carbpept.  
CC PRINTS; PR00724; CRBOXYPTASEC.  
CC ProDom; PD001189; Serine\_carbpept; 1.  
CC PROSITE; PS00131; CARBOXYPEPT\_SER\_SER; 1.  
CC PROSITE; PS00560; CARBOXYPEPT\_SER\_HIS; 1.  
CC Hydrolase; Carboxypeptidase; Glycoprotein; Zymogen; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT PROPEP 22 73 BY SIMILARITY.  
FT CHAIN 74 484 SERINE CARBOXYPEPTIDASE III.  
FT PROPEP 485 500 BY SIMILARITY.  
FT ACT\_SITE 216 216 BY SIMILARITY.  
FT ACT\_SITE 404 404 BY SIMILARITY.  
FT ACT\_SITE 461 461 BY SIMILARITY.  
FT BINDING 407 407 SUBSTRATE (BY SIMILARITY).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 500 AA; 55334 MW; B2ACE10EF8484CDA CRC64;

Query Match 72.0%; Score 36; DB 1; Length 500;  
Best Local Similarity 85.7%; Pred. No. 56;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9  
|||||:|

Db 167 TGTGFSY 173

RESULT 9  
CBP3\_HORVU  
ID CBP3\_HORVU STANDARD; PRT; 508 AA.

```
AC DT 01-MAY-1991 (Rel. 18, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine carboxypeptidase III precursor (EC 3.4.16.5) (CP-MIII).
GN CBP3 OR CXP;3.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya; TISSUE=Aleurone;
RA Rocher A., Lok F., Camerton-Mills V., von Wettstein D.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 81-491.
RP STRAIN=cv. Gula;
MEDLINE=90315015; PubMed=2639682;
RA Soerensen S.B., Svendsen I., Breddam K.;
RT "Primary structure of carboxypeptidase III from malted barley.";
RL Carlsberg Res. Commun. 54:193-202(1989).
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
CC broad specificity.
CC -!- ENZYME REGULATION: INHIBITED BY MERCURIC IONS.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE ENDOSPERM.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED MAINLY IN THE ALEURONE AND, TO A
CC LESSER EXTENT IN THE EMBRYO, THROUGHOUT THE 5-DAYS GERMINATION
CC PERIOD EXCLUSIVELY, WITH A MAXIMAL LEVEL AT 3 DAYS. ALSO FOUND IN
CC THE ROOTS AND SHOOTS OF THE GROWING SEEDLING.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
CC
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CC
CC EMBL: Y09604; CAA70817.1;
DR PIR: A35275; A35275.
DR HSP: P00729; ICPY.
DR MEROPS: S10.009; -.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00450; serine_carbpept.
DR PRINTS: PR00724; CRBOXPPTASEC.
DR ProDom: PD001189; Serine_carbpept; 1.
DR PROSITE: PS001131; CARBOXYPEPT_SER_SER; 1.
DR PROSITE: PS00560; CARBOXYPEPT_SER_HIS; 1.
DR KEGG: 0450; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 19
FT PROPEP 20 80
FT CHAIN 81 491
FT PROPEP 492 508
FT MOD_RES 81 81
FT ACT_SITE 223 223
FT ACT_SITE 411 411
FT ACT_SITE 468 468
FT BINDING 414 414
FT CARBOHYD 151 151
FT VARIANT 265 265
SQ SEQUENCE 508 AA; 56362 MW; 70C6751D78D40AB6 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 508;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TGTGFAY 9
|||||:

AC DT 01-MAY-1991 (Rel. 18, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine carboxypeptidase III precursor (EC 3.4.16.5) (CP-MIII).
GN CBP3 OR CXP;3.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya; TISSUE=Aleurone;
RA Rocher A., Lok F., Camerton-Mills V., von Wettstein D.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 81-491.
RP STRAIN=cv. Gula;
MEDLINE=90315015; PubMed=2639682;
RA Soerensen S.B., Svendsen I., Breddam K.;
RT "Primary structure of carboxypeptidase III from malted barley.";
RL Carlsberg Res. Commun. 54:193-202(1989).
CC -!- CATALYTIC ACTIVITY: Release of a C-terminal amino acid with a
CC broad specificity.
CC -!- ENZYME REGULATION: INHIBITED BY MERCURIC IONS.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE ENDOSPERM.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED MAINLY IN THE ALEURONE AND, TO A
CC LESSER EXTENT IN THE EMBRYO, THROUGHOUT THE 5-DAYS GERMINATION
CC PERIOD EXCLUSIVELY, WITH A MAXIMAL LEVEL AT 3 DAYS. ALSO FOUND IN
CC THE ROOTS AND SHOOTS OF THE GROWING SEEDLING.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10.
CC
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CC
CC EMBL: Y09604; CAA70817.1;
DR PIR: A35275; A35275.
DR HSP: P00729; ICPY.
DR MEROPS: S10.009; -.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00450; serine_carbpept.
DR PRINTS: PR00724; CRBOXPPTASEC.
DR ProDom: PD001189; Serine_carbpept; 1.
DR PROSITE: PS001131; CARBOXYPEPT_SER_SER; 1.
DR PROSITE: PS00560; CARBOXYPEPT_SER_HIS; 1.
DR KEGG: 0450; Carboxypeptidase; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 19
FT PROPEP 20 80
FT CHAIN 81 491
FT PROPEP 492 508
FT MOD_RES 81 81
FT ACT_SITE 223 223
FT ACT_SITE 411 411
FT ACT_SITE 468 468
FT BINDING 414 414
FT CARBOHYD 151 151
FT VARIANT 265 265
SQ SEQUENCE 508 AA; 56362 MW; 70C6751D78D40AB6 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 508;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TGTGFAY 9
|||||:

Db 174 TGTGFSY 180

RESULT 10
PHX5_MOUSE
ID PHX5_MOUSE STANDARD; PRT; 672 AA.
AC P08399;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Per-hexamer repeat protein 5.
GN PHXR5 OR PER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86014384; PubMed=2413365;
RA Shin H.S., Bargiello T.A., Clark B.T., Jackson F.R., Young M.W.;
RT "An unusual coding sequence from a Drosophila clock gene is conserved
RT in vertebrates.";
RL Nature 317:445-448(1985).
CC -!- SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.
CC
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CC
CC EMBL: M12039; AAA88320.1;
DR EMBL: X02966; CAA26710.1; ALT_INIT.
DR PIR: A24403; UMMS.
DR MGD: MGI:104521; Phxr5.
DR InterPro: IPR000561; EGF-like.
DR SMART: SM00181; EGF; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR Repeat.
KW DOMAIN 59 672 G-T REPEATS.
FT SEQUENCE 672 AA; 57924 MW; E85BF428CF424C0B CRC64;

Query Match 70.0%; Score 35; DB 1; Length 672;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RGTGTGFA 8
|||||:
Db 625 RGTGTGTA 632

RESULT 11
VP4_ROTFC
ID VP4_ROTFC STANDARD; PRT; 736 AA.
AC P26193;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8].
GN S3.
OS Porcine rotavirus (group C / strain Cowden).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10916;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92124743; PubMed=1310192;
RA Brenmont M., Juste-Lesage P., Chabanne-Vautherot D.,
RA Charpillienne A., Cohen J.;
RT "Sequences of the four larger proteins of a porcine group C rotavirus
RT and comparison with the equivalent group A rotavirus proteins.";
```

Virology 186:684-692(1992).  
 -!- SUBCELLULAR LOCATION: Outer capsid.  
 -!- PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE OTHER PRODUCT IS VP5.  
 -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.  
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 -----  
 EMBL; M74218; AAB00802.1; .  
 PIR; D40822; VPXRPC.  
 InterPro: IPR000416; Cap\_VP4.  
 Pfam; PF00426; VP4; 1.  
 Coat protein; Glycoprotein.  
 FT CHAIN 1 736  
 CHAIN 1 244  
 CHAIN 251 736  
 CARBOHYD 39 39  
 CARBOHYD 61 61  
 CARBOHYD 64 64  
 CARBOHYD 93 93  
 CARBOHYD 162 162  
 CARBOHYD 191 191  
 CARBOHYD 237 237  
 CARBOHYD 251 251  
 CARBOHYD 304 304  
 CARBOHYD 471 471  
 CARBOHYD 631 631  
 SQ SEQUENCE 736 AA; 83231 MW; 356F9226D5016577 CRC64;  
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 Query Match 70.08; Score 35; DB 1; Length 736;  
 Best Local Similarity 85.78; Pred. No. 1.2e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TGTGFAY 9  
 :|||||  
 DB 454 SGTGFAY 460  
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 RESULT 12  
 VILLI\_CHICK  
 ID VILLI\_CHICK STANDARD; PRT; 826 AA.  
 AC P02640;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 OS Villin.  
 OC Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88276884; PubMed=2839826;  
 RA Bazari W.L., Matsudaira P., Wallek M., Smeal T., Jakes R., Ahmed Y.;  
 RT "Villin sequence and peptide map identify six homologous domains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4986-4990(1988).  
 RN [2]  
 RP SEQUENCE OF 751-826.  
 RX MEDLINE=81264203; PubMed=6790532;  
 RA Glenney J.R. Jr., Geisler N., Kaulfus P., Weber K.;  
 RT "Demonstration of at least two different actin-binding sites in villin, a calcium-regulated modulator of F-actin organization.";  
 RL J. Biol. Chem. 256:8156-8161(1981).  
 RN [3]  
 RP SEQUENCE OF 751-826.  
 RX MEDLINE=83082892; PubMed=6848508;

RA Hesterberg L.K., Weber K.;  
 RT "Demonstration of three distinct calcium-binding sites in villin, a modulator of actin assembly.";  
 RL J. Biol. Chem. 258:365-369(1983).  
 RN [4]  
 RP STRUCTURE BY NMR OF 1-127.  
 RX MEDLINE=94191534; PubMed=8142900;  
 RA Markus M.A., Nakayama T., Matsudaira P., Wagner G.;  
 RT "Solution structure of villin 14T, a domain conserved among actin-severing proteins.";  
 RL Protein Sci. 3:70-81(1994).  
 RN [5]  
 RP STRUCTURE BY NMR OF 1-127.  
 RX MEDLINE=97337440; PubMed=9194180;  
 RA Markus M.A., Matsudaira P., Wagner G.;  
 RT "Refined structure of villin 14T and a detailed comparison with other actin-severing domains.";  
 RL Protein Sci. 6:1197-1209(1997).  
 RN [6]  
 RP STRUCTURE BY NMR OF 792-826.  
 RX MEDLINE=97307248; PubMed=9164455;  
 RA McKnight C.J., Matsudaira P.T., Kim P.S.;  
 RT "NMR structure of the 35-residue villin headpiece subdomain.";  
 RL Nat. Struct. Biol. 4:180-184(1997).  
 CC -!- FUNCTION: CA(2+)-REGULATED ACTIN-BINDING PROTEIN. ITS CAPPING ACTION IS LOCALIZED TO DOMAIN I; ITS SEVERING ACTION IS A COOPERATION BETWEEN AN F-ACTIN BINDING SITE OF DOMAIN II AND THE CAPPING ACTIVITY OF DOMAIN I.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- TISSUE SPECIFICITY: COMPONENT OF BRUSH BORDER MICROVILLI.  
 CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.  
 CC -!- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.  
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 -----  
 EMBL; J03781; AAA49133.1; .  
 PIR; A03082; A03082.  
 PIR; A31822; A31822.  
 PDB; 2VIL; 01-APR-97.  
 PDB; 2VIL; 01-APR-97.  
 PDB; 1VII; 12-AUG-97.  
 DR InterPro; IPR001974; Gelsolin.  
 DR InterPro; IPR003128; VHP.  
 DR Pfam; PF00626; Gelsolin; 6.  
 DR Pfam; PF02209; VHP; 1.  
 DR PRINTS; PR00597; GELSOLIN.  
 DR SMART; SM00262; GEL; 6.  
 DR SMART; SM00153; VHP; 1.  
 KW Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat;  
 KW 3D-structure.  
 FT DOMAIN 1 734  
 FT CORE.  
 FT HEADPIECE.  
 FT GELSOLIN-LIKE 1.  
 FT REPEAT 27 76  
 FT REPEAT 148 188  
 FT REPEAT 265 309  
 FT REPEAT 408 457  
 FT REPEAT 528 568  
 FT REPEAT 631 672  
 FT REPEAT 820 823  
 FT SITE 129 137  
 FT SITE 112 119  
 FT SITE 138 146  
 FT STRAND 21 23  
 FT STRAND 30 32  
 FT TURN 34 36

FT STRAND 39 41  
FT STRAND 44 44  
FT STRAND 47 53  
FT STRAND 58 64  
FT STRAND 68 68  
FT HELIX 72 88  
FT TURN 89 90  
FT STRAND 95 97  
FT STRAND 104 110  
FT TURN 112 113  
FT STRAND 116 118  
FT TURN 124 125  
SQ SEQUENCE 826 AA; 6A8898F7DF947389 CRC64;

Query Match 70.0%; Score 35; DB 1; Length 826;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 RGTGTGFAY 9  
| | | | | | |  
52 RKTGSGFSY 60

RESULT 13

CYC\_CHLRE STANDARD; PRT; 111 AA.

AC P15451;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cytochrome c.  
GN CYC1.  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=137C / CC-125, and cwl5;  
RX MEDLINE=89178731; PubMed=2853233;  
RA Amati B.B., Goldschmidt-Clermont M., Wallace C.J.A., Rochaix J.-D.;  
RT "cDNA and deduced amino acid sequences of cytochrome c from  
Chlamydomonas reinhardtii: unexpected functional and phylogenetic  
implications";  
RL J. Mol. Evol. 28:151-160(1988).  
RN [2]

SEQUENCE FROM N.A.  
STRAIN=137C / CC-125;  
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: Electron carrier protein. The oxidized form of the  
cytochrome c heme group can accept an electron from the heme group  
of the cytochrome c1 subunit of cytochrome reductase. Cytochrome c  
then transfers this electron to the cytochrome oxidase complex,  
the final protein carrier in the mitochondrial electron-transport  
chain.  
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
-!- PTM: Binds one heme group per molecule.  
-!- SIMILARITY: Belongs to the cytochrome c family.  
-----  
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EMBL; M35173; AAA33084.1; -;  
EMBL; Z99829; CAB16954.1; -;  
PIR; S29514; S29514.  
HSP; P00055; ICCR.  
InterPro; IPR000345; CytC\_heme\_bind.

DR InterPro; IPR003088; Cyt\_C1.  
DR InterPro; IPR002327; Cyt\_C1AB.  
DR Pfam; PF00034; cytochrome\_c\_1.  
DR PRINTS; PR00604; CYCHRMETCIAB.  
DR PRODOM; PD000375; Cyt\_C1AB; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; 1.  
KW Mitochondrion; Electron transport; Respiratory chain; Heme.  
FT INIT\_MET 0  
FT BINDING 22 22 HEME (COVALENT).  
FT BINDING 25 25 HEME (COVALENT).  
FT METAL 26 26 IRON (HEME AXIAL LIGAND).  
FT METAL 88 88 IRON (HEME AXIAL LIGAND).  
SQ SEQUENCE 111 AA; 11826 MW; 6F11A35EA71C7078 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 111;  
Best Local Similarity 75.0%; Pred. No. 30;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTGFAY 9  
| | | | | | |  
Db 49 GTAAGFAY 56

RESULT 14

YOD2\_CAEEL STANDARD; PRT; 233 AA.

AC P34594;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical 26.8 kDa protein ZC262.2 in chromosome III.  
GN ZC262.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,  
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,  
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
Parsons J., Percy C., Rifkin L., Ropra A., Saunders D., Showkeen R.,  
Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,  
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans";  
RL Nature 368:32-38(1994).  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; L23647; AAK29991.1; -;  
PIR; S44882; S44882.  
WormPep; ZC262.2; CE00350.  
KW Hypothetical protein.  
SQ SEQUENCE 233 AA; 26825 MW; 84F99FB67A6DD5D6 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 233;  
Best Local Similarity 66.7%; Pred. No. 60;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9  
||||| :  
Db 225 RGTGTGFAY 233

RESULT 15  
CCAS\_CHICK STANDARD; PRT; 281 AA.  
AC 042398;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Voltage-dependent L-type calcium channel alpha-1s subunit (Fragment).  
GN CALNALS.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
PP SEQUENCE FROM N.A.  
RT STRAIN=White leghorn; TISSUE=Intestinal epithelium;  
RT Xu J., Norman A.W., Henry H.L., de Bolland A.R., Zanillo L.P.;  
RT "Molecular characterization of an L-type calcium channel in chick  
RT intestinal epithelial cells";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THE ISOFORM ALPHA-1S GIVES RISE TO L-TYPE CALCIUM  
CC CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE  
CC "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY  
CC DIHYDROPYRIDINES (DHP), PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND  
CC BY OMEGA-AGATOXIN-IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER  
CC INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-  
CC AGATOXIN-IVA (OMEGA-AGA-IVA). CALCIUM CHANNELS CONTAINING THE  
CC ALPHA-1S SUBUNIT PLAY AN IMPORTANT ROLE IN EXCITATION- CONTRACTION  
CC COUPLING IN SKELETAL MUSCLE (BY SIMILARITY).  
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN  
CC ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE  
CC CHANNEL (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
CC -!- DOMAIN: THE LOOP BETWEEN REPEATS II AND III INTERACTS WITH THE  
CC RYANODINE RECEPTOR, AND IS THEREFORE IMPORTANT FOR CALCIUM RELEASE  
CC FROM THE ENDOPLASMIC RETICULUM NECESSARY FOR MUSCLE CONTRACTION  
CC (BY SIMILARITY).  
CC -!- PTM: PHOSPHORYLATION BY CAPK STIMULATES THE CALCIUM CHANNEL  
CC FUNCTION (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
CC FAMILY.

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-----  
EMBL; AF007877; AAB63206.1; .  
DR InterPro; IPR001682; Ca/Na\_pore.  
DR InterPro; IPR002077; Ca\_channel.  
DR InterPro; IPR002111; Ca\_channel\_TrpL.  
DR InterPro; IPR000836; M\_channel\_nlg.  
PFam; PF00520; Ion\_trans; 1.

DR PRINTS: PR00167: CACHANNEL.  
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
KW Calcium-binding; Phosphorylation.  
FT NON\_TER 1  
FT REPEAT <1 8 III.  
FT REPEAT 45 >281 IV.  
FT TRANSMEM <1 5 S6 OF REPEAT III (POTENTIAL).  
FT DOMAIN 6 58 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 59 77 S1 OF REPEAT IV (POTENTIAL).  
FT DOMAIN 78 92 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 93 112 S2 OF REPEAT IV (POTENTIAL).  
FT DOMAIN 113 120 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 121 139 S3 OF REPEAT IV (POTENTIAL).  
FT DOMAIN 140 152 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 153 171 S4 OF REPEAT IV (POTENTIAL).  
FT DOMAIN 172 190 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 191 210 S5 OF REPEAT IV (POTENTIAL).  
FT DOMAIN 211 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 >281 S6 OF REPEAT IV (POTENTIAL).  
FT BINDING <1 17 TO DIHYDROPYRIDINES (BY SIMILARITY).  
FT BINDING 258 >281 TO DIHYDROPYRIDINES (BY SIMILARITY).  
FT BINDING 270 >281 TO PHENYLALKYLAMINES (BY SIMILARITY).  
FT SITE 244 244 CALCIUM ION SELECTIVITY AND PERMEABILITY  
FT (BY SIMILARITY).  
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT NON\_TER 281 281  
SQ SEQUENCE 281 AA; 32729 MW; 46BE70FA44D9166B CRC64;

Query Match 68.0%; Score 34; DB 1; Length 281;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTGTFAY 9  
|||||  
Db 274 GTGTFAY 279

Search completed: February 14, 2003, 11:16:21  
Job time : 5.64516 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 : Search time 18.7258 Seconds  
(without alignments)  
99.030 Million cell updates/sec

Title: US-09-701-001B-3

Perfect score: 50

Sequence: 1 RGTGTGFAY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Matched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID  | Description        |
|------------|-------|---------------|--------|--------|--------------------|
| 1          | 41    | 82.0          | 416    | Q8XT81 | Q8xt81 ralstonia s |
| 2          | 39    | 78.0          | 644    | Q83342 | Q83342 murid herpe |
| 3          | 39    | 78.0          | 644    | Q41940 | Q41940 murid herpe |
| 4          | 39    | 78.0          | 685    | Q8RNT4 | Q8rnt4 pseudomonas |
| 5          | 39    | 78.0          | 685    | Q914G8 | Q914g8 pseudomonas |
| 6          | 37    | 74.0          | 266    | Q42245 | Q42245 brachydanio |
| 7          | 37    | 74.0          | 502    | Q8YVU9 | Q8yvu9 anabaena sp |
| 8          | 37    | 74.0          | 519    | Q93J30 | Q93j30 streptomyc  |
| 9          | 36    | 72.0          | 101    | Q41689 | Q41689 vigna radia |
| 10         | 36    | 72.0          | 146    | Q92TR3 | Q92tr3 hordeum vul |
| 11         | 36    | 72.0          | 150    | Q41601 | Q41601 triticum tu |
| 12         | 36    | 72.0          | 165    | Q40651 | Q40651 oryza sativ |
| 13         | 36    | 72.0          | 198    | Q8XIF4 | Q8xif4 clostridium |
| 14         | 36    | 72.0          | 360    | Q9M450 | Q9m450 cicer ariet |
| 15         | 36    | 72.0          | 401    | Q96ZK7 | Q96zk7 sulfolobus  |
| 16         | 36    | 72.0          | 423    | Q91201 | Q91201 pseudomonas |

|    |    |      |      |    |        |                    |
|----|----|------|------|----|--------|--------------------|
| 17 | 36 | 72.0 | 482  | 5  | Q9TY20 | Q9ty20 plasmodium  |
| 18 | 36 | 72.0 | 501  | 10 | Q9XH61 | Q9xh61 matricaria  |
| 19 | 36 | 72.0 | 1077 | 16 | Q92U15 | Q92u15 rhizobium m |
| 20 | 36 | 72.0 | 3295 | 16 | Q8ZIA8 | Q8zia8 versinia pe |
| 21 | 35 | 70.0 | 163  | 16 | Q90UH9 | Q90uh9 staphylococ |
| 22 | 35 | 70.0 | 398  | 16 | Q930R4 | Q930r4 rhizobium m |
| 23 | 35 | 70.0 | 401  | 16 | Q8YLY2 | Q8yly2 anabaena sp |
| 24 | 35 | 70.0 | 429  | 16 | Q8YLY2 | Q8yly2 anabaena sp |
| 25 | 35 | 70.0 | 440  | 16 | Q9RXX0 | Q9rxx0 streptomyce |
| 26 | 35 | 70.0 | 452  | 16 | P73354 | P73354 synechocyst |
| 27 | 35 | 70.0 | 563  | 4  | Q60398 | Q60398 homo sapien |
| 28 | 35 | 70.0 | 579  | 2  | Q8VLY0 | Q8vly0 treponema s |
| 29 | 35 | 70.0 | 733  | 12 | Q65525 | Q65525 bovine grou |
| 30 | 35 | 70.0 | 744  | 12 | Q82039 | Q82039 human rotav |
| 31 | 35 | 70.0 | 744  | 12 | Q82040 | Q82040 human rotav |
| 32 | 35 | 70.0 | 744  | 12 | Q933A0 | Q933a0 human rotav |
| 33 | 35 | 70.0 | 744  | 12 | Q99229 | Q992z9 human rotav |
| 34 | 35 | 70.0 | 744  | 12 | Q8V9B0 | Q8v9b0 human rotav |
| 35 | 35 | 70.0 | 747  | 4  | Q13311 | Q13311 homo sapien |
| 36 | 35 | 70.0 | 747  | 4  | Q9U188 | Q9u188 homo sapien |
| 37 | 35 | 70.0 | 758  | 5  | Q9NKT0 | Q9nkt0 leishmania  |
| 38 | 35 | 70.0 | 789  | 4  | Q9BQG5 | Q9bqg5 homo sapien |
| 39 | 35 | 70.0 | 2115 | 17 | Q8TQ00 | Q8tqn0 methanosarc |
| 40 | 34 | 68.0 | 41   | 2  | Q9ZG78 | Q9zg78 chlamydia t |
| 41 | 34 | 68.0 | 99   | 16 | Q9PEL0 | Q9pel0 xylella fas |
| 42 | 34 | 68.0 | 110  | 2  | Q9AQM8 | Q9aqm8 pseudomonas |
| 43 | 34 | 68.0 | 134  | 10 | Q9FKF5 | Q9fkf5 arabidopsis |
| 44 | 34 | 68.0 | 134  | 10 | Q945L5 | Q945l5 arabidopsis |
| 45 | 34 | 68.0 | 149  | 13 | Q8UVC7 | Q8uvc7 agkistrodon |

## ALIGNMENTS

RESULT 1  
Q8XT81  
ID Q8XT81 PRELIMINARY; PRT; 416 AA.  
AC Q8XT81;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Probable metabolite transport transmembrane protein.  
GN RSP0234 OR RS05189.  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OG Plasmid megaplasmid.  
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
OC Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000.  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
RA Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,  
RA Weissenbach J., Boucher C.A.;  
RL Nature 415:497-502(2002).  
RL "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
DR EMBL; AL646077; CAD17385.1; --  
DR InterPro; IPR003662; sub.transporter.  
DR Pfam; PF00083; sugar.tr; 1  
DR PROSITE; PS00216; SUGAR\_TRANSPORT\_1; UNKNOWN\_1.  
DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; UNKNOWN\_1.  
KW Plasmid; Complete proteome.  
SQ SEQUENCE 416 AA; 44052 MW; 4AC593FD3AC0EF4B CRC64;

Query Match 82.0%; Score 41; DB 16; Length 416;  
Best Local Similarity 77.8%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RGTGTGFAY 9

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Db 350 RGTGVCFCY 358
||||| ||| |
RESULT 2
Q83342
AC O83342 PRELIMINARY; PRT: 644 AA.
ID O83342;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Thymidine kinase.
OS murid herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=33708;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=G2.4;
RX MEDLINE=96213518; PubMed=8638414;
Pepper S.D., Stewart J.P., Arrand J.R., Mackett M.;
"Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and
glycoprotein H: sequence, expression, and characterization of
pyrimidine kinase activity.";
Virology 219:475-479(1996).
RT EMBL: X93468; CAA63755.1; -.
DR InterPro: IPR001889; TK_herpes.
DR Pfam: PF00693; TK_herpes; 1.
DR ProDom: PD001519; TK_herpes; 1.
KW Kinase.
SQ SEQUENCE 644 AA; 72256 MW; FDF782746EB557A9 CRC64;
Query Match 78.0%; Score 39; DB 12; Length 644;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTCFAY 9
|| ||||| |
Db 300 RGDGTGFRY 308

RESULT 3
Q41940
AC O41940 PRELIMINARY; PRT: 644 AA.
ID O41940;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Thymidine kinase.
OS murid herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=33708;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WUMS, AND G2.4;
RX MEDLINE=97366649; PubMed=9223479;
Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E.,
Dal Canto A.J., Speck S.H.;
"Complete sequence and genomic analysis of murine gammaherpesvirus
68.";
J. Virol. 71:5894-5904(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=WUMS;
RX Latreille P., Wamsley P., Waterston R.H.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=G2.4;
RX MEDLINE=96213518; PubMed=8638414;
Pepper S.D., Stewart J.P., Arrand J.R., Mackett M.;
"Murine gammaherpesvirus-68 encodes homologues of thymidine kinase and
glycoprotein H: sequence, expression, and characterization of
pyrimidine kinase activity.";
Virology 219:475-479(1996).
RT EMBL: X93468; CAA63755.1; -.
DR InterPro: IPR001889; TK_herpes.
DR Pfam: PF00693; TK_herpes; 1.
DR ProDom: PD001519; TK_herpes; 1.
KW Kinase.
SQ SEQUENCE 644 AA; 72256 MW; FDF782746EB557A9 CRC64;
Query Match 78.0%; Score 39; DB 12; Length 644;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTCFAY 9
|| ||||| |
Db 300 RGDGTGFRY 308

RESULT 4
Q8RNT4
ID Q8RNT4 PRELIMINARY; PRT: 685 AA.
AC Q8RNT4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Linoleate oxygen oxidoreductase.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=42A2 NCBI 40045;
RX Vidal-Mas J., Besumbes O., Manresa M., Busquets M.;
"Cloning, sequence and expression of a lipoygenase gene of
Pseudomonas aeruginosa 42A2 NCBI 40045.";
Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF479686; AAL85880.1; -.
SQ SEQUENCE 685 AA; 74572 MW; DA863B58A47C4C29 CRC64;
Query Match 78.0%; Score 39; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFCAY 9
|||||||
Db 305 TGTGFCAY 311

RESULT 5
Q9I4G8
ID Q9I4G8 PRELIMINARY; PRT: 685 AA.
AC Q9I4G8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Probable lipoygenase.
GN PALL69.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

```

```
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.D., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RL EMBL: AE004547; AAG04558.1; -.
DR HSP: P08170; 2SBL.
DR InterPro: IPR000907; Lipoxigenase.
DR Pfam: PF00305; lipoxigenase; 1.
DR PRINTS: PR00087; LIPOXYGENASE.
KW Complete proteome.
SQ SEQUENCE 685 AA; 74803 MW; B6A307595AE16A5E CRC64;

Query Match 78.0%; Score 39; DB 16; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGFAY 9
   |||||
Db 305 TGTGFAY 311

RESULT 6
O42245 PRELIMINARY; PRT; 266 AA.
AC O42245;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Atonal homologue-1.
GN ATOH1 OR ZATH-1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.-H., Bae Y.-K., Yamanaka Y., Yamashita S., Shimizu T., Fujii R.,
RA Hibi M., Hirano T.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
EMBL: AF024536; AAB82272.1; -.
DR ZFIN: ZDB-GENE-990415-17; atoh1.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00010; HLH; 1.
DR SMART: SM00353; HLH; 1.
SQ SEQUENCE 266 AA; 28786 MW; 56A92494B52FEFB8 CRC64;

Query Match 74.0%; Score 37; DB 13; Length 266;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
   |||||
Db 209 RGTGTGVYPY 217

RESULT 7
O8YVU9 PRELIMINARY; PRT; 502 AA.
AC O8YVU9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein A11875.
GN A11875.
```

```
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kato T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RA "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003587; BAB73574.1; -.
DR InterPro: IPR004843; M-peptidase.
DR InterPro: IPR004844; S/T-phosphatase.
DR Pfam: PF00149; Metallophos; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 502 AA; 57518 MW; A5F008CBC2C59E61 CRC64;

Query Match 74.0%; Score 37; DB 16; Length 502;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGTGTGFAY 9
   |||||
Db 159 RGTGTGEAY 167

RESULT 8
O93J30 PRELIMINARY; PRT; 519 AA.
ID O93J30;
AC O93J30;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative protease
GN SCO3977 OR SCBAC25E3.14.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Collins M., Harris D.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RA "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RA "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
```



DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Dehydrin.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoidae; Oryzaceae; Oryza.  
 OC NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McEvoy S.M., Sheoran I.S., Saini H.S.;  
 RT "A rice cDNA encoding a late embryogenesis abundant protein.";  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U60097; AAB03330.1; -;  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin.1.  
 DR PROSITE: PS00823; DEHYDRIN.2; 1.  
 DR SEQUENCE 165 AA; 16671 MW; 581218E22BE37043 CRC64;  
 Query Match 72.0%; Score 36; DB 10; Length 165;  
 Best Local Similarity 87.5%; Pred. No. 83;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GTGTGFAY 9  
 Db 116 GTGTGGAY 123  
 RESULT 13  
 Q8X1F4 PRELIMINARY; PRT; 198 AA.  
 AC Q8X1F4;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical protein CPE2167.  
 GN CPE2167.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 OC NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / TYPE A;  
 RX PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yanashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 flesh-eater."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL; AF003193; BAB81873.1; -;  
 DR Hypothetical protein; Complete proteome.  
 KW SEQUENCE 198 AA; 21538 MW; E5B6F630D8434332 CRC64;  
 SQ SEQUENCE 198 AA; 21538 MW; E5B6F630D8434332 CRC64;  
 Query Match 72.0%; Score 36; DB 16; Length 198;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGTGTGF 7  
 Db 74 KGTGTGF 80  
 RESULT 14  
 Q9M450 PRELIMINARY; PRT; 360 AA.  
 ID Q9M450;  
 AC Q9M450;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Serine carboxypeptidase (EC 3.4.16.6) (Fragment).  
 OS Cicer arietinum (Chickpea) (Garbanzo).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.  
 OC NCBI\_TaxID=3827;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;  
 RA Dopico B., Esteban R., Labrador E.;  
 RT "A serine carboxypeptidase is expressed in chickpea epicotyls.";  
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ271659; CAB1127.1; -;  
 DR HSSP; P08819; 1BCS.  
 DR MEROPS: S10.009; -;  
 DR InterPro: IPR001563; Serine\_carbpept.  
 DR Pfam: PF00450; serine\_carbpept; 1.  
 DR PRINTS: PK00724; CRBOXYPTASEC.  
 DR PRODOM: PD001189; Serine\_carbpept; 1.  
 DR PROSITE: PS00560; CARBOXYPEPT\_SER\_HIS; 1.  
 DR PROSITE: PS00131; CARBOXYPEPT\_SER\_SER; 1.  
 KW Carboxypeptidase; Hydrolase.  
 FT NON\_TER 1  
 SQ SEQUENCE 360 AA; 40153 MW; 140BEBACD0143FE0 CRC64;  
 Query Match 72.0%; Score 36; DB 10; Length 360;  
 Best Local Similarity 85.7%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TGTGFAY 9  
 Db 29 TGTGFAY 35  
 RESULT 15  
 Q96ZK7 PRELIMINARY; PRT; 401 AA.  
 ID Q96ZK7;  
 AC Q96ZK7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Putative transporter.  
 GN ST1828.  
 OS Sulfolobus tokodaii.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OC NCBI\_TaxID=111955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JCM 10545 / 7;  
 RX PubMed=11572479;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,  
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
 RA Ohshima T., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic thermoacidophilic  
 Crenarchaeon, Sulfolobus tokodaii strain 7.";  
 RL DNA Res. 8:123-140(2001).  
 DR EMBL; AP000987; BAB66918.1; -;  
 DR InterPro: IPR003662; sub.transporter.  
 DR Pfam: PF00083; sugar\_tr\_1.  
 DR PROSITE: PS00216; SUGAR\_TRANSPORT\_1; UNKNOWN\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 401 AA; 43730 MW; 73B08EA26463B17 CRC64;  
 Query Match 72.0%; Score 36; DB 17; Length 401;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 RGTGTGFAY 9  
 Db 336 RATGTGFAY 344

Fri Feb 14 15:00:54 2003

us-09-701-001b-3.rspt

Page 6

Search completed: February 14, 2003, 11:18:39  
Job time : 20.8925 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 : Search time 40.6452 Seconds  
(without alignments)  
49.176 Million cell updates/sec

Title: US-09-701-001B-4

Perfect score: 79

Sequence: 1 KASQSVYDGDGYNN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 79    | 100.0       | 15     | AA70195  | MAB 3B9 light chain |
| 2          | 79    | 100.0       | 15     | AAW3027  | Anti-Fas MAB HFE/A  |
| 3          | 79    | 100.0       | 15     | AA723772 | CDR of the light c  |
| 4          | 79    | 100.0       | 15     | AA18114  | Light chain CDR fo  |
| 5          | 79    | 100.0       | 15     | AA14744  | Mouse anti-Fas ant  |
| 6          | 79    | 100.0       | 15     | AAW90894 | Murine anti-Fas an  |
| 7          | 79    | 100.0       | 15     | AA59259  | Antibody 4H5 L cha  |
| 8          | 79    | 100.0       | 15     | AA51136  | Murine CD4/CD34 re  |
| 9          | 79    | 100.0       | 15     | ABB74863 | Humanised anti-Fas  |
| 10         | 79    | 100.0       | 15     | ABB74909 | Humanised anti-Fas  |

|    |    |       |     |          |                     |
|----|----|-------|-----|----------|---------------------|
| 11 | 79 | 100.0 | 19  | AA66143  | CD-4 antibody vari  |
| 12 | 79 | 100.0 | 103 | AA59263  | Antibody 4H5 L cha  |
| 13 | 79 | 100.0 | 103 | AA51140  | Murine derived pro  |
| 14 | 79 | 100.0 | 106 | AA33309  | MAE15 light chain.  |
| 15 | 79 | 100.0 | 106 | AA58197  | Light chain amino   |
| 16 | 79 | 100.0 | 111 | AA90541  | Immunoglobulin L c  |
| 17 | 79 | 100.0 | 111 | AA33305  | MAE11 light chain.  |
| 18 | 79 | 100.0 | 111 | AA55123  | Mouse anti-HIV mu5  |
| 19 | 79 | 100.0 | 111 | AA55127  | Mouse-human chimere |
| 20 | 79 | 100.0 | 111 | AA60302  | Anti HIV antibody   |
| 21 | 79 | 100.0 | 111 | AA60306  | Chimeric anti HIV   |
| 22 | 79 | 100.0 | 111 | AA23781  | Light chain variab  |
| 23 | 79 | 100.0 | 111 | AA18123  | Light chain sequen  |
| 24 | 79 | 100.0 | 111 | AAW5650  | Mus musculus anti-  |
| 25 | 79 | 100.0 | 111 | AA55193  | Light chain amino   |
| 26 | 79 | 100.0 | 111 | AA59267  | Antibody 4H5 L cha  |
| 27 | 79 | 100.0 | 111 | AA51144  | Murine derived pro  |
| 28 | 79 | 100.0 | 111 | AA51146  | Murine derived pro  |
| 29 | 79 | 100.0 | 111 | AA76939  | Variable light cha  |
| 30 | 79 | 100.0 | 112 | AA24575  | Human x mouse modi  |
| 31 | 79 | 100.0 | 113 | AA71895  | Monoclonal antibod  |
| 32 | 79 | 100.0 | 115 | AA04134  | Anti-Leu 3a light   |
| 33 | 79 | 100.0 | 120 | AA48618  | Sequence of the mo  |
| 34 | 79 | 100.0 | 131 | AA90543  | Amino acids sequen  |
| 35 | 79 | 100.0 | 131 | AA04132  | Anti-Leu 3a light   |
| 36 | 79 | 100.0 | 131 | AA75355  | Humanized antibody  |
| 37 | 79 | 100.0 | 131 | AA72022  | Humanized antibody  |
| 38 | 79 | 100.0 | 131 | AA23779  | Light chain variab  |
| 39 | 79 | 100.0 | 131 | AA23771  | Light chain variab  |
| 40 | 79 | 100.0 | 131 | AA18126  | Light chain sequen  |
| 41 | 79 | 100.0 | 131 | AA18118  | Light chain sequen  |
| 42 | 79 | 100.0 | 132 | AA70189  | Mouse MAB 3B9 ligh  |
| 43 | 79 | 100.0 | 132 | AA23767  | Light chain variab  |
| 44 | 79 | 100.0 | 132 | AA18120  | Light chain sequen  |
| 45 | 79 | 100.0 | 218 | AAW13563 | Humanised anti-L-s  |

## ALIGNMENTS

RESULT 1  
AA70195  
ID AA70195 standard; Protein; 15 AA.  
XX  
AC AA70195;  
XX 20-SEP-1995 (first entry)  
DT MAB 3B9 light chain CDR.  
XX  
DE Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; MAB; interleukin-4; IL-4; allergy; CDR;  
KW complementarity determining region.  
XX  
OS Mus sp.  
XX  
PN WO9507301-A.  
XX  
PD 16-MAR-1995.  
XX  
PF 07-SEP-1994; 94WO-US10308.  
XX  
PR 07-SEP-1993; 93US-0117366.  
PR 14-OCT-1993; 93US-0136783.  
XX  
(SMIK ) SMITHKLINE BEECHAM CORP.  
(SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Gross MS, Holmes SD, Sylvester DR;  
XX WPI; 1995-123387/16.  
XX  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions

PS Disclosure; Page 54; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pGEM7f+ and transformed into E. coli  
 CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that  
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were  
 CC identified.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDDYDGD SYMN 15

|||||

1 KASQSVDDYDGD SYMN 15

RESULT 2

AAW83027

ID AAW83027 standard; Peptide; 15 AA.

XX AC AAW83027;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-Fas MAB HFE7A light chain CDR-I1.

XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

KW apoptosis; autoimmune disease; Hashimoto's disease;

KW systemic lupus erythematosus; graft versus host disease;

KW Sjogren syndrome; pernicious anaemia; Addison's disease;

KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;

KW rheumatoid arthritis; autoimmune haemolytic anaemia;

KW myasthenia gravis; multiple sclerosis; Basedow's disease;

KW thrombopenia purpura; insulin-dependent diabetes; allergy;

KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

KW transplant rejection; therapy; complementarity determining region;

KW CDR.

XX OS Mus musculus.

XX AU9859701-A.

XX PD 08-OCT-1998.

XX PF 30-MAR-1998; 98AU-0059701.

XX PR 08-OCT-1997; 97JP-0276064.

XX PR 01-APR-1997; 97JP-0082953.

XX PR 25-JUN-1997; 97JP-0169088.

XX PA (SANY ) SANKYO CO LTD.

XX AKio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX XX WPI; 1998-543440/47.

XX XX

PT New antibodies and proteins bind conserved epitope of Fas antigen -

PT used to evaluate drugs in animal models and to treat Fas-associated

PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,

PT myocarditis, hepatitis and AIDS

XX Claim 9; Page 184; 292pp; English.

CC This is the amino acid of complementarity determining region 1  
 CC (CDR-I1) of the light chain (see AAW83042) of murine anti-human Fas  
 CC monoclonal antibody HFE7A. The invention relates to antibodies,  
 CC especially humanised antibodies (see AAW83031-37), recognising the  
 CC Fas antigen. Such antibodies preferably comprise a heavy chain and  
 CC a light chain including CDRs (see AAW83024-29) from the heavy and  
 CC light chains of HFE7A. Humanised antibodies are produced by CDR  
 CC grafting. The antibodies are capable of inducing apoptosis in  
 CC abnormal cells expressing Fas, and of inhibiting Fas-induced  
 CC apoptosis in normal cells. They are used to evaluate, in animal  
 CC models, treatments of diseases that involve Fas/Fas ligand  
 CC interactions, and also to treat such diseases, including autoimmune  
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's  
 CC disease, thrombopenia purpura and insulin-dependent diabetes),  
 CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and  
 CC transplant rejection (all claimed).

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 19; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVDDYDGD SYMN 15

|||||

1 KASQSVDDYDGD SYMN 15

RESULT 3

AAV23772

ID AAV23772 standard; Peptide; 15 AA.

XX AC AAV23772;

XX DT 13-SEP-1999 (first entry)

XX DE CDR of the light chain variable region of antibody 3B9.

XX KW Light chain variable region; Interleukin-4; IL-4; antibody 3B9;

XX chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;

XX Immunoglobulin E-mediated allergic reaction; allergic rhinitis; shock;

XX conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;

XX rheumatoid arthritis; host-versus-graft disease; renal disease;

XX allergy; complementarity determining region.

XX OS Mus sp.

XX US5928904-A.

XX PD 27-JUL-1999.

XX PF 07-JUN-1995; 95US-0483632.

XX PR 07-JUN-1995; 95US-0483632.

XX PR 07-SEP-1993; 93US-0117366.

XX PR 14-OCT-1993; 93US-0136783.

XX PR 07-SEP-1994; 94WO-US10308.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX FA (SMIK ) SMITHKLINE BEECHAM PLC.

XX XX Gross MS, Holmes SD, Sylvester DR;

XX XX WPI; 1999-429500/36.

XX DR N-PSDB; AAX85889.

XX XX

PT New DNA molecules encoding recombinant antibodies useful for

PT treating IL4-mediated conditions



XX Example 3; Column 43-44; 50pp; English.

XX The present sequence represents a complementarity determining region

XX (CDR) of the light chain variable region of murine interleukin-4

XX (IL-4) antibody 389. The specification describes chimeric and

XX humanised IL-4 monoclonal antibodies. The antibodies of the

XX invention are used in therapeutic and pharmaceutical compositions

XX for treating IL-4 mediated and immunoglobulin E-mediated allergic

XX reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,

XX atopic asthma, anaphylactic shock, rheumatoid arthritis,

XX host-versus-graft disease and renal disease. They are also useful

XX in the diagnosis of an allergy or condition associated with excess

XX IL-4 production through the measurement e.g. by ELISA of circulating

XX endogenous IL-4 levels in humans.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15

DB 1 KASQSVYDYGDSYMN 15

|||||

RESULT 4

AA18114

ID AAY18114 standard; peptide; 15 AA.

XX AAY18114;

XX 11-AUG-1999 (first entry)

DE Light chain CDR for hIL-4 specific antibody.

XX Antibody; Interleukin-4; IL4; Immunoglobulin E; IgE mediated disease;

XX allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

XX atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

XX autoimmune disease; graft versus host disease;

XX complementarity determining region; CDR.

XX Synthetic.

XX US914110-A.

22-JUN-1999.

PF 07-JUN-1995; 95US-0483636.

PR 07-JUN-1995; 95US-0483636.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-370482/31.

DR N-PSDB; AAX79513.

XX Recombinant IL4 antibodies

PS Claim 7; Column 43; 50pp; English.

XX This sequence represents a light chain complementarity determining region

XX (CDR) from an antibody of the invention. The antibody is a chimeric or

XX humanised interleukin-4 (IL4) monoclonal antibody for the treatment of

XX immunoglobulin E (IgE) mediated diseases. The antibodies are useful for

XX the treatment of allergic disorders such as allergic rhinitis,

CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.

CC The antibodies are also useful for regulating B and T cell proliferation

CC and as such are useful in the treatment of autoimmune diseases and graft

CC versus host disease.

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15

DB 1 KASQSVYDYGDSYMN 15

|||||

RESULT 5

AA14744

ID AAB14744 standard; peptide; 15 AA.

XX AAB14744;

XX 24-NOV-2000 (first entry)

DE Mouse anti-Fas antibody HFE7A light chain CDR1.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

XX murine; complementarity determining region; CDR; human Fas;

XX Fas ligand; apoptosis modulator; programmed cell death;

XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;

XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;

XX hepatitis; AIDS; graft rejection; light chain.

XX Mus musculus.

XX JP2000169393-A.

XX 20-JUN-2000.

PF 30-SEP-1999; 99JP-0278301.

XX 30-SEP-1998; 98JP-0276883.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2000-485645/43.

DR Preventive or treating agent for the diseases caused by an abnormality

PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains

PT anti-Fas antibody .

XX Claim 10; Page 65; 139pp; Japanese.

PS The invention relates to compositions for the prevention or treatment

XX or diseases caused by an abnormality in the Fas/Fas ligand system

CC containing an anti-Fas antibody as the active component. The anti-Fas

CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,

CC or a humanised version of HFE7A containing identical CDRs

CC (complementarity determining regions) to antibody HFE7A. Via its

CC interaction with Fas, the antibody of the invention acts as a modulator

CC of apoptosis. The composition of the invention may therefore be used in

CC the treatment or prevention of conditions such as autoimmune diseases,

CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS

CC and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3

CC of the light chain of the murine anti-human Fas monoclonal antibody

CC HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

XX Sequence 15 AA;

Query Match 100.0%; Score 79; DB 21; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGDSDYMN 15  
 |||||  
 Db 1 KASQSVVDYDGDSDYMN 15

RESULT 6  
 AA90894  
 ID AA90894 standard; peptide; 15 AA.  
 AC AA90894;  
 XX  
 XX 08-AUG-2000 (first entry)  
 DE Murine anti-Fas antibody peptide fragment #4.  
 XX  
 XX Fas; antibody: murine; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Mus musculus.  
 XX EP990663-A2.  
 PN  
 XX  
 PD 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI; 2000-258930/23.  
 DR  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Disclosure; Page 98; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a murine anti-Fas antibody peptide fragment described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGDSDYMN 15  
 |||||  
 Db 1 KASQSVVDYDGDSDYMN 15

RESULT 7  
 AA59259  
 ID AA59259 standard; peptide; 15 AA.  
 AC AA59259;  
 XX  
 XX 17-APR-2000 (first entry)  
 DT  
 XX Antibody 4H5 L chain variable region CDR1 fragment.  
 DE  
 XX CD4 antigen; anti-human; antibody; 4H5; drug; CDR;  
 KW complementarity determining region.  
 KW  
 OS Mus sp.  
 XX  
 XX JP11332563-A.  
 PN  
 XX 07-DEC-1999.  
 PD  
 XX 26-MAY-1998; 98JP-0163034.  
 PF  
 XX 26-MAY-1998; 98JP-0163034.  
 PR  
 XX (ASAH ) ASahi KASEI KOGYO KK.  
 PA  
 XX WPI; 2000-091351/08.  
 DR  
 XX  
 XX An antibody and the nucleic acid coding the antibody -  
 PT  
 XX Claim 2; Page 14; 25pp; Japanese.  
 PS  
 XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. Sequences  
 CC AA59259-61 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the  
 CC antibody 4H5 respectively.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGDSDYMN 15  
 |||||  
 Db 1 KASQSVVDYDGDSDYMN 15

RESULT 8  
 AA51136  
 ID AA51136 standard; Protein; 15 AA.  
 AC AA51136;  
 XX  
 XX 31-MAR-2000 (first entry)  
 DT

XX DE Murine CD4/CD34 recognizing antibody light chain CDR-1 region #1.  
 XX KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; complementarity determining region;  
 KW CDR-1; light chain; murine.  
 XX OS Mus sp.  
 XX PN WO9961629-A1.  
 XX PD 02-DEC-1999.  
 XX PF 24-MAY-1999; 99WO-JP02711.  
 XX PR 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 (ASAH ) ASAH KASEI KOGYO KK.  
 (ASAH ) ASAH MEDICAL CO LTD.  
 XX Ono M, Soka T, Morimoto I, Miyamura K;  
 PI WPI; 2000-086720/07.  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX Claim 3; Page 76; 11lpp; Japanese.  
 XX This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived complementarity determining  
 CC region CDR-1 protein fragment which is used to illustrate the method of  
 CC the invention.  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KASQSVYDGDSDSYMN 15  
 | | | | | | | | | | | | | | |  
 Db 1 KASQSVYDGDSDSYMN 15  
 | | | | | | | | | | | | | | |  
 RESULT 9  
 ABB74863  
 ID ABB74863 standard; Peptide; 15 AA.  
 XX AC ABB74863;  
 XX 26-APR-2002 (first entry)  
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 29.  
 XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
 KW autoimmune disease; allergy; atopic.  
 XX OS Homo sapiens.  
 XX JP2001342148-A.  
 PN 11-DEC-2001.  
 XX

XX 28-MAR-2001; 2001JP-0093106.  
 XX 29-MAR-2000; 2000JP-0090918.  
 XX (SANY ) SANKYO CO LTD.  
 XX WPI; 2002-145113/19.  
 XX Drug containing humanised anti-Fas antibody, used for preventing and  
 PT treating autoimmune diseases, allergy, and atopy -  
 XX Example 6 (Preparatory); Page 26; 194pp; Japanese.  
 XX The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in Fas/Fas ligand system containing as the active  
 CC component an antibody having as the light chain subunit a polypeptide  
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
 CC fully defined in the specification and having an activity of combining  
 CC specifically with mammalian Fas and an activity of inducing apoptosis  
 CC in a cell expressing Fas. The agent has immunosuppressive and  
 CC antiallergic activity and is used for preventing and treating autoimmune  
 CC diseases, allergy, atopy and others. The present sequence is that of a  
 CC peptide, useful to the invention.  
 XX SQ Sequence 15 AA;  
 Query Match 100.0%; Score 79; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 1.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KASQSVYDGDSDSYMN 15  
 | | | | | | | | | | | | | | |  
 Db 1 KASQSVYDGDSDSYMN 15  
 | | | | | | | | | | | | | | |  
 RESULT 10  
 ABB74909  
 ID ABB74909 standard; Peptide; 15 AA.  
 XX AC ABB74909;  
 XX 30-APR-2002 (first entry)  
 XX Humanised anti-Fas antibody related peptide SEQ ID NO 26.  
 XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;  
 KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;  
 KW autoimmune disease; allergy; atopy.  
 XX OS Homo sapiens.  
 XX JP2001342149-A.  
 PN 11-DEC-2001.  
 XX 28-MAR-2001; 2001JP-0093243.  
 XX 29-MAR-2000; 2000JP-0091144.  
 XX (SANY ) SANKYO CO LTD.  
 XX WPI; 2002-145114/19.  
 XX Drug for preventing or treating e.g. autoimmune disease or allergy,  
 PT comprises humanised anti-Fas antibody -  
 XX Example 6 (preparatory); Page 26; 154pp; Japanese.  
 XX The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in the Fas/Fas ligand system containing, as the  
 CC active component, an antibody having a light chain subunit and a heavy

CC chain subunit and an activity of combining specifically with mammalian  
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The  
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is  
 CC used for preventing and treating autoimmune diseases, allergy, atopy and  
 CC others. The present sequence is that of a peptide useful to the  
 CC invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15  
 |||||  
 Db 1 KASQSVVDYDGD SYMN 15

RESULT 11

AAR66143  
 AAR66143 standard; peptide; 19 AA.

AAR66143;

XX 12-JUL-1995 (first entry)

DE CD-4 antibody variable region complementary peptide.

CC CD-4 antibody variable region; complementary peptide;  
 KW extra-corporeal blood circulation; cell filter material.

XX Synthetic.

XX JP06269663-A.

XX 27-SEP-1994.

XX 17-MAR-1993; 93JP-0057206.

XX 17-MAR-1993; 93JP-0057206.

XX (TOYM ) TOYOCO KK.

XX WPI; 1994-346316/43.

XX Material for collecting cells positive for CD-4 antibody -  
 PT comprises nonwoven fabric having keto-alkyl halide functional gp

XX Example 1; Page 6; 9pp; Japanese.

CC AAR66140-R66146 are peptides complementary to the variable region  
 CC of the CD-4 antibody, these peptides are fixed onto a claimed  
 CC nonwoven fabric (average fibre dia. of 1-30 microns) coated with  
 CC keto-alkyl halide functional groups. This material can be used  
 CC as a filter for CD-4 positive cells in a medical treatment  
 CC involving the extra-corporeal circulation of blood.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 79; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15  
 |||||  
 Db 5 KASQSVVDYDGD SYMN 19

RESULT 12

AA59263  
 ID AA59263 standard; protein; 103 AA.

XX AAY59263;

XX 17-APR-2000 (first entry)  
 DT Antibody 4H5 L chain variable region.  
 XX CD4 antigen; anti-human; antibody; 4H5; drug.  
 KW Mus sp.

XX JPL1332563-A.

XX 07-DEC-1999.

XX 26-MAY-1998; 98JP-0163034.

XX 26-MAY-1998; 98JP-0163034.

XX (ASAH ) ASAH KASEI KOGYO KK.

XX WPI: 2000-091351/08.

XX N-PSDB; AA258662.

XX An antibody and the nucleic acid coding the antibody -  
 PT Claim 5; Page 15-16; 25pp; Japanese.

XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the L chain variable region of the antibody 4H5.

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 79; DB 21; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVVDYDGD SYMN 15

Db 16 KASQSVVDYDGD SYMN 30

RESULT 13

AA51140

ID AAY51140 standard; Protein; 103 AA.

XX AAY51140;

XX 31-MAR-2000 (first entry)

XX Murine derived protein fragment #2.

CC Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.

XX Mus sp.

XX WO9961629-A1.

XX 02-DEC-1999.

XX 24-MAY-1999; 99WO-JP02711.

XX 25-MAY-1998; 98JP-0159957.

XX 26-MAY-1998; 98JP-0163023.

XX (ASAH ) ASAH KASEI KOGYO KK.

XX (ASAH ) ASAH MEDICAL CO LTD.

XX Ono M, Soka T, Morimoto I, Miyamura K;

XX WPI: 2000-086720/07.

Fri Feb 14 15:00:54 2003

DR N-PSDB; AA444204.  
XX Devices containing antibodies recognising CD4 or CD34 and their use for  
PT the separation of CD4 or CD34 positive cells  
XX  
XX  
PS Claim 22; Page 79; 11pp; Japanese.  
XX  
XX This invention describes a novel device (I) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived protein fragment which is used  
CC to illustrate the method of the invention.  
XX

Sequence 103 AA;  
Query Match 100.0%; Score 79; DB 21; Length 103;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMN 15  
DB 16 KASQSVYDGDSDYMN 30

RESULT 14  
AAR33309  
ID AAR33309 standard; Protein: 106 AA.

XX AAR33309;  
AC AAR33309;  
XX 05-JUL-1993 (first entry)  
XX MAE15 light chain.  
XX Antibody; high affinity; FCEH; low affinity; FCEH;  
KW IgE receptor; histamine; mast cell; basophil; Kabat;  
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.  
XX Synthetic.  
OS WO9304173-A.  
PN 04-MAR-1993.

PF 14-AUG-1992; 92WO-US06860.  
XX 14-AUG-1991; 91US-0744768.  
PR 07-MAY-1992; 92US-0879495.

XX (GETH ) GENENTECH INC.  
XX Jardieu PM, Presta LG;  
PI WPI; 1993-094004/11.  
XX Polypeptide(s) binding to specific Fc epsilon receptors - act as  
PT IgE antagonists; useful for treating and preventing IgE-mediated  
PT disorders e.g. allergies  
XX Disclosure; Fig 2; 11pp; English.

XX Antibodies capable of binding FCEH-bound IgE but which are  
CC substantially incapable of binding FCEH-bound IgE or inducing  
CC histamine release from mast cells or basophils, comprise a human  
CC Kabat CDR domain into which has been substituted a positionally  
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE  
CC antibodies MAE11, MAE13, MAE15 or MAE17.  
XX

SQ Sequence 106 AA;

Query Match 100.0%; Score 79; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMN 15  
DB 24 KASQSVYDGDSDYMN 38

RESULT 15  
AAY85197  
ID AAY85197 standard; protein: 106 AA.

XX AAY85197;  
AC AAY85197;  
XX 29-JUN-2000 (first entry)  
XX Light chain amino acid sequence of mouse antibody MAE15.

XX Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEH; FCEH;  
KW low affinity binding receptor; high affinity binding receptor; allergy;  
KW diagnosis; treatment; histamine release; prevent; light chain.

OS Mus sp.  
XX US6037453-A.  
PN 14-MAR-2000.

PF 06-JUN-1995; 95US-0466151.  
XX 15-MAR-1995; 95US-0405617.  
PR 14-AUG-1992; 92WO-US06860.

XX 26-JAN-1994; 94US-0185899.  
XX (GETH ) GENENTECH INC.  
XX Presta LG, Jardieu PM;  
PI WPI; 2000-269913/23.

XX New bispecific antibodies, useful for treating immunoglobulin  
PT E-mediated disease, binds to IgE, but only when on the low affinity  
PT receptor, and to an antigen other than IgE  
XX Claim 1; Fig 2; 48pp; English.

XX This sequence represents the light chain amino acid sequence of a mouse  
CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a  
CC bispecific antibody that binds specifically to IgE when IgE is bound to  
CC its low affinity receptor (FCEH), but does not bind to IgE, when IgE is  
CC bound to its high affinity receptor (FCEH). The bispecific antibody  
CC comprises an IgE-binding arm with human framework residues of a recipient  
CC human antibody and donor murine CDR (complementarity determining region)  
CC residues, but with at least one human CDR residue replacing the analogous  
CC murine residue. The antibody also comprises an Fv that is specific for a  
CC predetermined antigen other than IgE. The antibodies work by displacing  
CC bound IgE from its receptor, or via competitive inhibition of its  
CC binding. The bispecific antibodies are used for diagnosis, treatment and  
CC prevention of allergy and other IgE-mediated diseases, also, when  
CC immobilised, for the isolation of FCEH from cells (for research or  
CC therapy). The bispecific antibodies of the invention do not cause  
CC granulation or release of histamine from mast cells.  
XX

SQ Sequence 106 AA;

Query Match 100.0%; Score 79; DB 21; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMN 15

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Page 8

Db        24 KASQSVXDGD SYM 38  
          |||||

Search completed: February 14, 2003, 11:15:44  
Job time : 41.6452 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 ; Search time 13.5484 Seconds  
(without alignments)  
32.575 Million cell updates/sec

Title: US-09-701-001B-4  
Perfect score: 79  
Sequence: 1 KASQSDYDGDGMN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 79    | 100.0       | 15     | 2     | US-08-483-636-16  |
| 2          | 79    | 100.0       | 15     | 2     | US-08-483-632-16  |
| 3          | 79    | 100.0       | 106    | 3     | US-08-466-151-6   |
| 4          | 79    | 100.0       | 106    | 4     | US-08-466-163B-6  |
| 5          | 79    | 100.0       | 111    | 1     | US-08-491-845-8   |
| 6          | 79    | 100.0       | 111    | 1     | US-08-491-845-16  |
| 7          | 79    | 100.0       | 111    | 2     | US-08-483-636-73  |
| 8          | 79    | 100.0       | 111    | 2     | US-08-483-632-73  |
| 9          | 79    | 100.0       | 111    | 3     | US-08-887-352B-5  |
| 10         | 79    | 100.0       | 111    | 3     | US-08-466-151-2   |
| 11         | 79    | 100.0       | 111    | 4     | US-09-109-207C-5  |
| 12         | 79    | 100.0       | 111    | 4     | US-09-296-005-5   |
| 13         | 79    | 100.0       | 111    | 4     | US-08-466-163B-2  |
| 14         | 79    | 100.0       | 115    | 3     | US-08-513-968-51  |
| 15         | 79    | 100.0       | 120    | 1     | US-08-111-080-24  |
| 16         | 79    | 100.0       | 120    | 1     | US-08-211-980-24  |
| 17         | 79    | 100.0       | 120    | 5     | PCT-US93-07967-24 |
| 18         | 79    | 100.0       | 131    | 2     | US-08-483-636-14  |
| 19         | 79    | 100.0       | 131    | 2     | US-08-483-636-58  |
| 20         | 79    | 100.0       | 131    | 2     | US-08-483-632-14  |
| 21         | 79    | 100.0       | 131    | 2     | US-08-483-632-58  |
| 22         | 79    | 100.0       | 131    | 4     | US-08-579-378A-14 |
| 23         | 79    | 100.0       | 131    | 4     | US-08-579-378A-18 |
| 24         | 79    | 100.0       | 132    | 2     | US-08-483-636-2   |
| 25         | 79    | 100.0       | 132    | 2     | US-08-483-632-2   |
| 26         | 79    | 100.0       | 218    | 5     | PCT-US96-13152-2  |
| 27         | 76    | 96.2        | 111    | 2     | US-08-887-352B-6  |

|    |    |      |     |   |                   |                   |
|----|----|------|-----|---|-------------------|-------------------|
| 28 | 76 | 96.2 | 111 | 4 | US-09-109-207C-6  | Sequence 6, Appli |
| 29 | 76 | 96.2 | 111 | 4 | US-09-296-005-6   | Sequence 6, Appli |
| 30 | 76 | 96.2 | 114 | 2 | US-08-887-352B-10 | Sequence 10, Appl |
| 31 | 76 | 96.2 | 114 | 4 | US-09-109-207C-10 | Sequence 10, Appl |
| 32 | 76 | 96.2 | 114 | 4 | US-09-296-005-10  | Sequence 10, Appl |
| 33 | 76 | 96.2 | 218 | 2 | US-08-887-352B-13 | Sequence 13, Appl |
| 34 | 76 | 96.2 | 218 | 3 | US-08-466-151-9   | Sequence 9, Appli |
| 35 | 76 | 96.2 | 218 | 4 | US-09-109-207C-13 | Sequence 13, Appl |
| 36 | 76 | 96.2 | 218 | 4 | US-09-296-005-13  | Sequence 13, Appl |
| 37 | 76 | 96.2 | 218 | 4 | US-08-466-163B-9  | Sequence 9, Appli |
| 38 | 73 | 92.4 | 41  | 3 | US-08-984-277-5   | Sequence 5, Appli |
| 39 | 73 | 92.4 | 239 | 2 | US-08-553-497A-18 | Sequence 18, Appl |
| 40 | 72 | 91.1 | 114 | 2 | US-08-887-352B-9  | Sequence 9, Appli |
| 41 | 69 | 87.3 | 114 | 4 | US-09-109-207C-9  | Sequence 9, Appli |
| 42 | 69 | 87.3 | 114 | 4 | US-09-296-005-9   | Sequence 9, Appli |
| 43 | 53 | 67.1 | 114 | 2 | US-08-887-352B-8  | Sequence 8, Appli |
| 44 | 53 | 67.1 | 218 | 4 | US-09-282-505-1   | Sequence 1, Appli |
| 45 | 53 | 67.1 | 218 | 4 | US-09-054-255-1   | Sequence 1, Appli |

ALIGNMENTS

RESULT 1  
US-08-483-636-16  
; Sequence 16, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

### RESULT 3

RESULT 4  
 US-08-466-163B-6  
 Sequence 6, Application US/08466163B  
 Patent No. 6329509  
 GENERAL INFORMATION:  
 APPLICANT: Jardiue, Paula M  
 APPLICANT: Prestia, Leonard G.  
 TITLE OF INVENTION: Immunoglobulin Variants  
 FILE REFERENCES: P0718P2C1D1  
 CURRENT APPLICATION NUMBER: US/08/466, 163B  
 CURRENT FILING DATE: 1995-06-06  
 PRIOR APPLICATION NUMBER: US 08/405,617



us-09-701-001b-4.rai

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; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 6  
 ; LENGTH: 106  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-08-466-163B-6

Query Match 100.0%; Score 79; DB 4; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KASQSDYDGD SYNM 15  
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 24 KASQSDYDGD SYNM 38

RESULT 5  
 US-08-491-845-8  
 ; Sequence 8, Application US/08491845  
 ; Patent No. 5773247  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAEDA, Hiroaki  
 ; APPLICANT: KIMACHI, Kazuhiko  
 ; APPLICANT: EDA, Yasuyuki  
 ; APPLICANT: SHIOSAKI, Kouichi  
 ; APPLICANT: OSATOMI, Kiyoshi  
 ; APPLICANT: TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Browdy and Neimark  
 ; STREET: 419 Seventh Street N.W. Ste. 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/491,845  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION NUMBER: PCT/JP93/00039  
 ; FILING DATE: 14-JAN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Browdy, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: MAEDA=5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 628-5197  
 ; TELEFAX: (202) 737-3528  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 111 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-491-845-8

Query Match 100.0%; Score 79; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KASQSDYDGD SYNM 15  
 |||||  
 Db 24 KASQSDYDGD SYNM 38

RESULT 6  
 US-08-491-845-16  
 ; Sequence 16, Application US/08491845  
 ; Patent No. 5773247  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAEDA, Hiroaki  
 ; APPLICANT: KIMACHI, Kazuhiko  
 ; APPLICANT: EDA, Yasuyuki  
 ; APPLICANT: SHIOSAKI, Kouichi  
 ; APPLICANT: OSATOMI, Kiyoshi  
 ; APPLICANT: TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Browdy and Neimark  
 ; STREET: 419 Seventh Street N.W. Ste. 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/491,845  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION NUMBER: PCT/JP93/00039  
 ; FILING DATE: 14-JAN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Browdy, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: MAEDA=5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 628-5197  
 ; TELEFAX: (202) 737-3528  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 111 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-491-845-16

Query Match 100.0%; Score 79; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDYDGD SYNM 15  
 |||||  
 Db 24 KASQSDYDGD SYNM 38

RESULT 7  
 US-08-483-636-73  
 ; Sequence 73, Application US/08483636  
 ; Patent No. 5914110  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holmes, Stephen D.  
 ; APPLICANT: Gross, Mitchell S.  
 ; APPLICANT: Sylvester, Daniel R.  
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

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; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5090
; TELEFAX: (215) 270-5024
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-483-636-73

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Query Match 100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KASQSVVDYDGDSDYMN 15
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DB 24 KASQSVVDYDGDSDYMN 38

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RESULT 8
US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-483-632-73

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Query Match 100.0%; Score 79; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KASQSVVDYDGDSDYMN 15
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DB 24 KASQSVVDYDGDSDYMN 38

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RESULT 9
US-08-887-352B-5
; Sequence 5, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489

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us-09-701-001b-4.ra1

Fri Feb 14 15:00:54 2003

TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-887-352B-5

Query Match 100.0%; Score 79; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15  
Db 24 KASQSVYDGDGYM 38

RESULT 10  
US-08-466-151-2  
Sequence 2, Application US/08466151  
Patent No. 6037453

GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 08-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
APPLICATION DATA: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P2C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-2

Query Match 100.0%; Score 79; DB 3; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15  
Db 24 KASQSVYDGDGYM 38

RESULT 11  
US-09-109-207C-5  
Sequence 5, Application US/09109207C  
Patent No. 6172213

GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P112381  
CURRENT APPLICATION NUMBER: US/09/109,207C  
CURRENT FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/051,554  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 44  
SEQ ID NO 5  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-109-207C-5

Query Match 100.0%; Score 79; DB 4; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15  
Db 24 KASQSVYDGDGYM 38

RESULT 12  
US-09-296-005-5  
Sequence 5, Application US/09296005  
Patent No. 6290957

GENERAL INFORMATION:  
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
FILE REFERENCE: P1123C1f  
CURRENT APPLICATION NUMBER: US/09/296,005  
CURRENT FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 08/887,352  
EARLIER FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 5  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-296-005-5

Query Match 100.0%; Score 79; DB 4; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYM 15  
Db 24 KASQSVYDGDGYM 38

RESULT 13  
US-08-466-163B-2  
Sequence 2, Application US/08466163B  
Patent No. 6329509

GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06

;; PRIOR APPLICATION NUMBER: US 08/405,617  
;; PRIOR FILING DATE: 1995-03-15  
;; PRIOR APPLICATION NUMBER: US 08/185,899  
;; PRIOR FILING DATE: 1994-01-26  
;; PRIOR APPLICATION NUMBER: US 07/879,495  
;; PRIOR FILING DATE: 1992-05-07  
;; PRIOR APPLICATION NUMBER: US 07/744,768  
;; PRIOR FILING DATE: 1991-08-14  
;; NUMBER OF SEQ ID NOS: 64  
;; SEQ ID NO 2  
;; LENGTH: 111  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-08-466-163B-2

Query Match 100.0%; Score 79; DB 4; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGD SYM 15  
|||||  
Db 24 KASQSDVDYDGD SYM 38

RESULT 14  
US-08-513-968-51  
; Sequence 51, Application US/08513968  
; Patent No. 6114143  
; GENERAL INFORMATION:  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: MAKIZUMI, Keiichi  
; APPLICANT: SHIOSAKI, Kouichi  
; APPLICANT: OSATOMI, Kiyoshi  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: HIGUCHI, Hirofumi  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,968  
; FILING DATE: 11-SEP-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 78913/1993  
; FILING DATE: 11-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: EDA=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 115 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-513-968-51

Query Match 100.0%; Score 79; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGD SYM 15  
|||||  
Db 28 KASQSDVDYDGD SYM 42

RESULT 15  
US-08-111-080-24  
; Sequence 24, Application 08/111080  
; Patent No. 5558865  
; GENERAL INFORMATION:  
; APPLICANT: Ohno, Tsuneya  
; TITLE OF INVENTION: HIV Immunotherapeutics  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: 08/111,080  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/748,562  
; FILING DATE: 22-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07111  
; FILING DATE: 24-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/039,457  
; FILING DATE: 22-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 31629  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-111-080-24

Query Match 100.0%; Score 79; DB 1; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDYDGD SYM 15  
|||||  
Db 24 KASQSDVDYDGD SYM 38

Search completed: February 14, 2003, 11:20:49  
Job time : 14.5484 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 ; Search time 8.70968 Seconds  
(without alignments)  
44.001 Million cell updates/sec

Title: US-09-701-001B-4  
Perfect score: 79  
Sequence: 1 KASQVDYDGDSTWN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

140259 seqs, 2554876 residues  
Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications-AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
|------------|-------|-------------|--------|-------|------------------|
| 1          | 79    | 100.0       | 15     | 9     | US-09-879-461-16 |
| 2          | 79    | 100.0       | 106    | 10    | US-09-802-077-6  |
| 3          | 79    | 100.0       | 106    | 10    | US-09-802-096-6  |
| 4          | 79    | 100.0       | 111    | 10    | US-09-802-077-2  |
| 5          | 79    | 100.0       | 111    | 10    | US-09-802-096-2  |
| 6          | 79    | 100.0       | 111    | 10    | US-09-920-171-5  |
| 7          | 79    | 100.0       | 131    | 9     | US-09-879-461-14 |
| 8          | 79    | 100.0       | 131    | 9     | US-09-879-461-58 |
| 9          | 79    | 100.0       | 132    | 9     | US-09-879-461-2  |
| 10         | 79    | 100.0       | 218    | 10    | US-09-917-410-2  |
| 11         | 79    | 100.0       | 238    | 9     | US-09-903-327A-4 |
| 12         | 76    | 96.2        | 111    | 10    | US-09-920-171-6  |
| 13         | 76    | 96.2        | 114    | 10    | US-09-920-171-10 |
| 14         | 76    | 96.2        | 218    | 10    | US-09-802-077-9  |
| 15         | 76    | 96.2        | 218    | 10    | US-09-802-096-9  |
| 16         | 76    | 96.2        | 218    | 10    | US-09-920-171-13 |
| 17         | 69    | 87.3        | 114    | 10    | US-09-920-171-9  |
| 18         | 50    | 63.3        | 114    | 10    | US-09-920-171-8  |
| 19         | 50    | 63.3        | 218    | 10    | US-09-920-171-15 |

|    |      |      |     |    |                   |
|----|------|------|-----|----|-------------------|
| 20 | 50   | 63.3 | 218 | 10 | US-09-920-171-17  |
| 21 | 50   | 63.3 | 218 | 10 | US-09-920-171-19  |
| 22 | 50   | 63.3 | 218 | 10 | US-09-920-171-24  |
| 23 | 50   | 63.3 | 248 | 10 | US-09-920-171-22  |
| 24 | 50   | 63.3 | 248 | 10 | US-09-920-171-23  |
| 25 | 46   | 58.2 | 134 | 10 | US-09-881-823-2   |
| 26 | 45   | 57.0 | 111 | 10 | US-09-920-171-7   |
| 27 | 42   | 53.2 | 269 | 12 | US-10-027-770-2   |
| 28 | 42   | 53.2 | 269 | 12 | US-10-027-770-5   |
| 29 | 41.5 | 52.5 | 222 | 9  | US-09-479-614-26  |
| 30 | 41.5 | 52.5 | 242 | 9  | US-09-479-614-20  |
| 31 | 41   | 51.9 | 112 | 9  | US-09-144-886-80  |
| 32 | 41   | 51.9 | 112 | 9  | US-09-144-886-81  |
| 33 | 41   | 51.9 | 112 | 9  | US-09-144-886-84  |
| 34 | 41   | 51.9 | 112 | 9  | US-09-144-886-85  |
| 35 | 41   | 51.9 | 112 | 9  | US-09-144-886-94  |
| 36 | 41   | 51.9 | 112 | 10 | US-09-810-502-36  |
| 37 | 41   | 51.9 | 112 | 10 | US-09-810-502-37  |
| 38 | 41   | 51.9 | 172 | 9  | US-09-854-133-111 |
| 39 | 41   | 51.9 | 172 | 10 | US-09-738-973-111 |
| 40 | 40.5 | 51.3 | 100 | 10 | US-09-840-459-22  |
| 41 | 40.5 | 51.3 | 112 | 9  | US-10-032-482-8   |
| 42 | 40.5 | 51.3 | 112 | 10 | US-09-772-120-6   |
| 43 | 40.5 | 51.3 | 112 | 10 | US-09-840-459-54  |
| 44 | 40.5 | 51.3 | 112 | 10 | US-09-840-459-58  |
| 45 | 40.5 | 51.3 | 535 | 9  | US-09-968-851-38  |

ALIGNMENTS

RESULT 1  
US-09-879-461-16  
; Sequence 16, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; Swedeland Rd.  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,461  
; FILING DATE: 12-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,929  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/136,783  
; FILING DATE: 14-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:

; AFFARIANI, FIESCA, LEONARD G.  
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)

;; PRIORITY APPLICATION NUMBER: US 07/744,768  
;; PRIORITY FILING DATE: 1991-08-14  
;; NUMBER OF SEQ ID NOS: 64  
;; SEQ ID NO 2  
;; LENGTH: 111  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-802-096-2

Query Match 100.0%; Score 79; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGSYMN 15  
Db 24 KASQSVDDYDGSYMN 38

ULT 6  
;; Sequence 5, Application US/09920171  
;; Patent No. US20020054878A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Lowman, Henry B.  
;; APPLICANT: Presta, Leonard G.  
;; APPLICANT: Jardiou, Paula M.  
;; APPLICANT: Lowe, John  
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)  
;; FILE REFERENCE: P1123C2US  
;; CURRENT APPLICATION NUMBER: US/09/920,171  
;; CURRENT FILING DATE: 2001-08-01  
;; PRIORITY APPLICATION NUMBER: US 08/887,352  
;; PRIORITY FILING DATE: 1997-07-02  
;; PRIORITY APPLICATION NUMBER: US 09/296,005  
;; PRIORITY FILING DATE: 1999-04-21  
;; NUMBER OF SEQ ID NOS: 44  
;; SEQ ID NO 5  
;; LENGTH: 111  
;; TYPE: PRT  
;; ORGANISM: Mus musculus  
US-09-920-171-5

Query Match 100.0%; Score 79; DB 10; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KASQSVDDYDGSYMN 15  
24 KASQSVDDYDGSYMN 38

RESULT 7  
US-09-879-461-14  
;; Sequence 14, Application US/09879461  
;; Publication No. US20020193575A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Holmes, Stephen D.  
;; Sylvester, Daniel R.  
;; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
;; Treatment of IL4 Mediated Disorders  
;; NUMBER OF SEQUENCES: 58  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corporation  
;; STREET: Corporate Intellectual Property, UW2220 - 709  
;; CITY: King of Prussia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19406-2799  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/879,461  
;; FILING DATE: 12-Jun-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: 08/612,929  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 08/136,783  
;; FILING DATE: 14-OCT-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/09/879,461  
FILING DATE: 12-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,929  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/136,783  
FILING DATE: 14-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: P50186-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5090  
FAX: (215) 270-5024  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-879-461-14

Query Match 100.0%; Score 79; DB 9; Length 131;  
Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGSYMN 15  
Db 43 KASQSVDDYDGSYMN 57

RESULT 8  
US-09-879-461-58  
;; Sequence 58, Application US/09879461  
;; Publication No. US20020193575A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Holmes, Stephen D.  
;; Gross, Mitchell S.  
;; Sylvester, Daniel R.  
;; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
;; Treatment of IL4 Mediated Disorders  
;; NUMBER OF SEQUENCES: 58  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corporation  
;; STREET: Corporate Intellectual Property, UW2220 - 709  
;; CITY: King of Prussia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19406-2799  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/879,461  
;; FILING DATE: 12-Jun-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: 08/612,929  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 08/136,783  
;; FILING DATE: 14-OCT-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-09-879-461-58

Query Match 100.0%; Score 79; DB 9; Length 131;  
Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
|||||

Db 43 KASQSVYDGDSDSYMN 57  
|||||

ILT 9

US-09-879-461-2  
Sequence 2, Application US/09879461  
Publication No. US2002019375A1  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
Gross, Mitchell S.  
Sylvester, Daniel R.  
TITLE OF INVENTION: Recombinant IL4 Antibodies useful in  
Treatment of IL4 Mediated Disorders  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: Corporate Intellectual Property, UW2220 - 709  
Swedeland Rd.  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,461  
FILING DATE: 12-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,929  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/136,783  
FILING DATE: 14-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090

SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-879-461-2

Query Match 100.0%; Score 79; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
|||||

Db 44 KASQSVYDGDSDSYMN 58  
|||||

RESULT 10

US-09-917-410-2  
Sequence 2, Application US/09917410  
Patent No. US20020098183A1  
GENERAL INFORMATION:  
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;  
CO, Man S.  
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF  
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR  
PREVENTION OF ACUTE ORGAN DAMAGE AFTER  
EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Computer Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/917,410  
FILING DATE: 26-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/578,953  
FILING DATE: <Unknown>

APPLICATION NUMBER: EP 95 114 969.9  
FILING DATE: 19-Sep-95  
ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. US20020098183Alman D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: ROER 1059-PFF/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 218  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-917-410-2

Query Match 100.0%; Score 79; DB 10; Length 218;  
Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
|||||

Db 24 KASQSVYDGDSDSYMN 38  
|||||

RESULT 11

US-09-903-327A-4  
Sequence 4, Application US/09903327A  
Patent No. US20020164333A1  
GENERAL INFORMATION:  
APPLICANT: Nemerow, Glen R.  
APPLICANT: Li, Erquang  
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR



;; TITLE OF INVENTION: GENE  
;; TITLE OF INVENTION: DELIVERY  
;; FILE REFERENCE: 22908-1228  
;; CURRENT APPLICATION NUMBER: US/09/903,327A  
;; CURRENT FILING DATE: 2001-07-10  
;; PRIOR APPLICATION NUMBER: 09/613,017  
;; PRIOR FILING DATE: 2000-07-10  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 4  
;; LENGTH: 238  
;; TYPE: PRT  
;; ORGANISM: Mouse  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (0)...(0)  
;; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody  
US-09-903-327A-4

Query Match 100.0%; Score 79; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 9.1e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:|||||  
Db 44 KASQSVYDYGDSYMN 58

## RESULT 12

US-09-920-171-6

; Sequence 6, Application US/09920171

; Patent No. US20020054878A1

; GENERAL INFORMATION:

; APPLICANT: Lowman, Henry B.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Lowe, John

; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)

; CURRENT APPLICATION NUMBER: US/09/920,171

; CURRENT FILING DATE: 2001-08-01

; PRIOR APPLICATION NUMBER: US 08/887,352

; PRIOR FILING DATE: 1997-07-02

; PRIOR APPLICATION NUMBER: US 09/296,005

; PRIOR FILING DATE: 1999-04-21

; NUMBER OF SEQ ID NOS: 44

; SEQ ID NO 6

; LENGTH: 111

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: F(ab) light chain sequence derived from MAE11

US-09-920-171-6

Query Match 96.2%; Score 76; DB 10; Length 111;  
Best Local Similarity 93.3%; Pred. No. 1.3e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:|||||  
Db 24 RASQSVYDYGDSYMN 38

## RESULT 13

US-09-920-171-10

; Sequence 10, Application US/09920171

; Patent No. US20020054878A1

; GENERAL INFORMATION:

; APPLICANT: Lowman, Henry B.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Lowe, John

; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)

;; FILE REFERENCE: P1123C2US  
;; CURRENT APPLICATION NUMBER: US/09/920,171  
;; CURRENT FILING DATE: 2001-08-01  
;; PRIOR APPLICATION NUMBER: US 08/887,352  
;; PRIOR FILING DATE: 1997-07-02  
;; PRIOR APPLICATION NUMBER: US 09/296,005  
;; PRIOR FILING DATE: 1999-04-21  
;; NUMBER OF SEQ ID NOS: 44  
;; SEQ ID NO 10  
;; LENGTH: 114  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-920-171-10

Query Match 96.2%; Score 76; DB 10; Length 114;  
Best Local Similarity 93.3%; Pred. No. 1.3e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:|||||  
Db 24 RASQSVYDYGDSYMN 38

## RESULT 14

US-09-802-077-9

; Sequence 9, Application US/09802077

; Patent No. US20010033842A1

; GENERAL INFORMATION:

; APPLICANT: Presta, Leonard G.

; APPLICANT: Jardieu, Paula M.

; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

; FILE REFERENCE: P0718P2C2US

; CURRENT APPLICATION NUMBER: US/09/802,077

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: US 08/405,617

; PRIOR FILING DATE: 1995-03-15

; PRIOR APPLICATION NUMBER: US 08/185,899

; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860

; PRIOR FILING DATE: 1992-08-14

; PRIOR APPLICATION NUMBER: US 07/879,495

; PRIOR FILING DATE: 1992-05-07

; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 9

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: humanized maell, version 1, light chain

US-09-802-077-9

Query Match 96.2%; Score 76; DB 10; Length 218;  
Best Local Similarity 93.3%; Pred. No. 2.5e-05;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:|||||  
Db 24 RASQSVYDYGDSYMN 38

## RESULT 15

US-09-802-096-9

; Sequence 9, Application US/09802096

; Patent No. US20010038839A1

; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amen

; FILE REFERENCE: P0718P2C3US

```

; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1, light chain
US-09-802-096-9

```

```

; Query Match 96.2%; Score 76; DB 10; Length 218;
; Best Local Similarity 93.3%; Pred No. 2.5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KASQSVYDGDGYMN 15
Db 24 RASQSVYDGDGYMN 38

```

Search completed: February 14, 2003, 11:21:31  
Job time : 8.70968 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 : Search time 15 Seconds  
(without alignments)  
96.134 Million cell updates/sec

Title: US-09-701-001B-4  
Perfect score: 79  
Sequence: 1 KASQSVDDYDGSYNN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 79    | 100.0       | 81     | 2 S42193 | Ig kappa chain V r |
| 2          | 79    | 100.0       | 93     | 2 A38601 | Ig kappa chain V r |
| 3          | 79    | 100.0       | 111    | 1 KVMS43 | Ig kappa chain V r |
| 4          | 79    | 100.0       | 111    | 1 KVMS83 | Ig kappa chain V r |
| 5          | 79    | 100.0       | 111    | 1 KVMS08 | Ig kappa chain V r |
| 6          | 79    | 100.0       | 111    | 1 KVMS69 | Ig kappa chain V r |
| 7          | 76    | 96.2        | 110    | 1 KVMS10 | Ig kappa chain V r |
| 8          | 76    | 96.2        | 112    | 2 S1971  | Ig kappa chain V r |
| 9          | 76    | 96.2        | 131    | 2 PH1226 | Ig kappa chain pre |
| 10         | 73    | 92.4        | 111    | 2 S09966 | Ig kappa chain V-J |
| 11         | 68    | 86.1        | 111    | 1 KVMS01 | Ig kappa chain V r |
| 12         | 65    | 82.3        | 112    | 2 S19976 | Ig kappa chain V r |
| 13         | 51    | 64.6        | 112    | 2 S19972 | Ig kappa chain V r |
| 14         | 48    | 60.8        | 282    | 2 A10948 | hypothetical prote |
| 15         | 46    | 58.2        | 96     | 2 B49442 | Ig light chain V r |
| 16         | 45    | 57.0        | 109    | 2 PH0093 | Ig kappa chain V r |
| 17         | 43    | 54.4        | 551    | 2 T03793 | calmodulin-binding |
| 18         | 42    | 53.2        | 102    | 2 PH1079 | Ig light chain V r |
| 19         | 42    | 53.2        | 111    | 1 KVMS80 | Ig kappa chain V r |
| 20         | 42    | 53.2        | 111    | 2 S09969 | Ig kappa chain V-J |
| 21         | 42    | 53.2        | 115    | 2 S63596 | Ig kappa chain V r |
| 22         | 42    | 53.2        | 120    | 2 S06732 | Ig kappa chain pre |
| 23         | 42    | 53.2        | 303    | 2 A83958 | Integrase/recombin |
| 24         | 41    | 51.9        | 91     | 2 S25462 | Ig kappa chain V r |
| 25         | 41    | 51.9        | 107    | 2 S26343 | Ig kappa chain V r |
| 26         | 41    | 51.9        | 107    | 2 S26344 | Ig kappa chain V r |
| 27         | 41    | 51.9        | 108    | 1 KVMS54 | Ig kappa chain V r |
| 28         | 41    | 51.9        | 111    | 1 KVMS37 | Ig kappa chain V r |
| 29         | 41    | 51.9        | 111    | 2 S09963 | Ig kappa chain V-J |

ALIGNMENTS

RESULT 1

S42193

Ig kappa chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 07-Oct-1994 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999

C:Accession: S42193

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42193

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 181 <MOI>

A:Cross-references: EMBL:Z25456; NID:9407846; PIDN:CAA80943.1; PID:9407847

A:Note: the authors translated the codon GTT for residue 36 as Ala

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 79; DB 2; Length 81;

Best Local Similarity 100.0%; Pred. No. 3.3e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGSYNN 15

Db 6 KASQSVDDYDGSYNN 20

RESULT 2

A38601

Ig kappa chain V region (IG3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999

C:Accession: A38601

R:Goshorn, S.C.; Retzel, E.; Jermerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti

A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: A38601

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-93 <GOS>

A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 79; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 3.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDYDGSYNN 15

|||||



Db 24 KASQSLDYDGD SYMN 38

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light

Db 24 KASQSLDYDGDSYMN 38

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-94/Domain: immunoglobulin homology <IMM>  
 F:23-92/Disulfide bonds: #status predicted

Query Match 86.1%; Score 68; DB 1; Length 111;  
 Best Local Similarity 86.7%; Pred. No. 0.00031;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
 ||||| |||||  
 DB 24 KASQSVDTGESYMN 38

## RESULT 12

S19976

Ig kappa chain V region (M-T413) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S19976

A:Description: Structural characterization of CD4 mAb.  
 A:Reference number: S19963

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 &lt;WEI&gt;

A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 82.3%; Score 65; DB 2; Length 112;  
 Best Local Similarity 80.0%; Pred. No. 0.001;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
 ||||| |||||  
 DB 24 KASQSLDYDADSYMH 38

## RESULT 13

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)

C>Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S19972

A:Description: Structural characterization of CD4 mAb.  
 A:Reference number: S19963

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 &lt;WEI&gt;

A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 64.6%; Score 51; DB 2; Length 112;  
 Best Local Similarity 66.7%; Pred. No. 0.22;  
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
 ||||| |||||  
 DB 24 KASQSVYDYNASVYMH 38

## RESULT 14

AI0948

hypothetical protein STY3863 [imported] - Salmonella enterica subsp. enterica serovar  
 C:Species: Salmonella enterica subsp. enterica serovar typhi  
 A:Note: this species has also been called Salmonella typhi  
 C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
 C:Accession: AI0948  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
 th, T.; Conner, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
 S.; Mole, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A&gt;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608

A:Accession: AI0948

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-282 &lt;PAR&gt;

A:Cross-references: GB:AL513382; PIDN:CAD09611.1; PID:g16504722; GSPDB:GN00176

C:Genetics:

A:Gene: STY3863

Query Match 60.8%; Score 48; DB 2; Length 282;  
 Best Local Similarity 60.0%; Pred. No. 1.8;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
 :| : ||||| |||  
 DB 263 EALEPDDYDGDYMN 277

## RESULT 15

B49442

Ig light chain V region (50.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C:Accession: B49442

R:Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapié, L.M.

Proteins 14, 499-508, 1992

A&gt;Title: Crystallization, sequence, and preliminary crystallographic data for an anti

A:Reference number: A49442; MUID:93066166; PMID:1438187

A:Accession: B49442

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-96 &lt;STU&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:8-86/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 58.2%; Score 46; DB 2; Length 96;  
 Best Local Similarity 53.3%; Pred. No. 1.3;  
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15  
 :||: ||| |||: |||  
 DB 16 RASESVDDGNSFLH 30

Search completed: February 14, 2003, 11:19:47  
 Job time : 16 secs

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 7.74194 Seconds  
(without alignments)  
80.360 Million cell updates/sec

Title: US-09-701-001b-4  
Perfect score: 79  
Sequence: 1 KASQSDVDGDSYMN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1          | 79    | 100.0         | 111    | 1     | KV3M_MOUSE  |
| 2          | 79    | 100.0         | 111    | 1     | KV3N_MOUSE  |
| 3          | 79    | 100.0         | 111    | 1     | KV3Q_MOUSE  |
| 4          | 79    | 100.0         | 111    | 1     | KV3O_MOUSE  |
| 5          | 76    | 96.2          | 110    | 1     | KV3P_MOUSE  |
| 6          | 68    | 86.1          | 111    | 1     | KV3L_MOUSE  |
| 7          | 45    | 57.0          | 111    | 1     | KV3C_MOUSE  |
| 8          | 43    | 54.4          | 682    | 1     | KIF2_XENLA  |
| 9          | 42    | 53.2          | 111    | 1     | KV3A_MOUSE  |
| 10         | 42    | 53.2          | 112    | 1     | KV3B_MOUSE  |
| 11         | 41    | 51.9          | 108    | 1     | KV3V_MOUSE  |
| 12         | 41    | 51.9          | 111    | 1     | KV3H_MOUSE  |
| 13         | 41    | 51.9          | 111    | 1     | KV3J_MOUSE  |
| 14         | 41    | 51.9          | 111    | 1     | KV3K_MOUSE  |
| 15         | 41    | 51.9          | 131    | 1     | KV3I_MOUSE  |
| 16         | 41    | 51.9          | 459    | 1     | CCMH_HAEIN  |
| 17         | 40    | 50.6          | 112    | 1     | KV3G_MOUSE  |
| 18         | 40    | 50.6          | 171    | 1     | ALL8_OLEEU  |
| 19         | 40    | 50.6          | 679    | 1     | KIF2_HUMAN  |
| 20         | 40    | 50.6          | 716    | 1     | KIF2_MOUSE  |
| 21         | 39.5  | 50.0          | 133    | 1     | KV2F_HUMAN  |
| 22         | 39    | 49.4          | 334    | 1     | VE2_BPV4    |
| 23         | 39    | 49.4          | 409    | 1     | TH1L_PANTH  |
| 24         | 39    | 49.4          | 638    | 1     | PDA4_MOUSE  |
| 25         | 39    | 49.4          | 643    | 1     | PDA4_RAT    |
| 26         | 38.5  | 48.7          | 75     | 1     | LSM6_SCHPO  |
| 27         | 38    | 48.1          | 83     | 1     | IBB3_SOYBN  |
| 28         | 38    | 48.1          | 123    | 1     | YI31_CAEEL  |
| 29         | 38    | 48.1          | 230    | 1     | DAG_ANTMA   |
| 30         | 38    | 48.1          | 243    | 1     | LP5B_LYTP1  |
| 31         | 38    | 48.1          | 260    | 1     | CABV_BOVIN  |
| 32         | 38    | 48.1          | 272    | 1     | TYPH_MYCHO  |
| 33         | 38    | 48.1          | 315    | 1     | CALU_HUMAN  |

|    |      |      |      |   |            |
|----|------|------|------|---|------------|
| 34 | 38   | 48.1 | 321  | 1 | LP5A_LYTP1 |
| 35 | 38   | 48.1 | 369  | 1 | VE2_HPV66  |
| 36 | 38   | 48.1 | 407  | 1 | YK95_CAEEL |
| 37 | 38   | 48.1 | 512  | 1 | VC02_VACCC |
| 38 | 38   | 48.1 | 512  | 1 | VC02_VACCV |
| 39 | 38   | 48.1 | 823  | 1 | YNS2_CAEEL |
| 40 | 38   | 48.1 | 1173 | 1 | TSP1_XENLA |
| 41 | 38   | 48.1 | 1592 | 1 | YHD5_YEAST |
| 42 | 37.5 | 47.5 | 80   | 1 | LSM6_HUMAN |
| 43 | 37.5 | 47.5 | 113  | 1 | KV2B_HUMAN |
| 44 | 37.5 | 47.5 | 350  | 1 | Y4RW_HUISN |
| 45 | 37   | 46.8 | 80   | 1 | YV6A_VIBCH |

|        |             |
|--------|-------------|
| P09485 | lytechinus  |
| Q80958 | human papil |
| P34311 | caenorhabdi |
| P21037 | vaccinia vi |
| P17371 | vaccinia vi |
| P34586 | caenorhabdi |
| P35448 | xenopus lae |
| P38735 | saccharomyc |
| Q9Y4V8 | homo sapien |
| P01615 | homo sapien |
| P55646 | rhizobium s |
| P58093 | vibrio chol |

## ALIGNMENTS

|   |                                |
|---|--------------------------------|
| RESULT 1  |                                |
| KV3M_MOUSE  |                                |
| ID KV3M_MOUSE   | STANDARD; PRT; 111 AA.         |
| AC P01665;  |                                |
| DT 21-JUL-1986 (Rel. 01, Created)                                     |                                |
| DT 21-JUL-1986 (Rel. 01, Last sequence update)                        |                                |
| DT 15-JUL-1999 (Rel. 38, Last annotation update)                      |                                |
| DE Ig kappa chain V-III region PC 7043.                               |                                |
| OS Mus musculus (Mouse).  |                                |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;            |                                |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |                                |
| OX NCBI_TaxID=10090;  |                                |
| RN [1]  |                                |
| RP SEQUENCE.  |                                |
| RX MEDLINE=79073152; PubMed=103003;                                   |                                |
| RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;         |                                |
| RT "Rearrangement of genetic information may produce immunoglobulin   |                                |
| RT diversity.";   |                                |
| RL Nature 276:785-790(1978).  |                                |
| DR PIR; A01937; KVM543.   |                                |
| DR HSSP; P80362; IWTL.  |                                |
| DR InterPro; IPR003006; Ig_MHC.                                       |                                |
| DR InterPro; IPR003596; Ig_v.   |                                |
| DR Pfam; PF00047; Ig; 1.  |                                |
| DR SMART; SM00406; IGV; 1.  |                                |
| DR Immunoglobulin V region.   |                                |
| KW DOMAIN 1 23  |                                |
| FT DOMAIN 24 38   | FRAMEWORK-1.                   |
| FT DOMAIN 39 53   | COMPLEMENTARITY-DETERMINING-1. |
| FT DOMAIN 54 60   | FRAMEWORK-2.                   |
| FT DOMAIN 61 92   | COMPLEMENTARITY-DETERMINING-2. |
| FT DOMAIN 93 101  | FRAMEWORK-3.                   |
| FT DOMAIN 102 111   | COMPLEMENTARITY-DETERMINING-3. |
| FT DISULFID 23 92   | FRAMEWORK-4.                   |
| FT NON_TER 111 111  | BY SIMILARITY.                 |
| SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;                 |                                |

Query Match 100.0%; Score 79; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.le-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMN 15

Db 24 KASQSDVDGDSYMN 38

## RESULT 2

|  |                        |
|--|------------------------|
| KV3N_MOUSE   |                        |
| ID KV3N_MOUSE  | STANDARD; PRT; 111 AA. |
| AC P01666;   |                        |
| DT 21-JUL-1986 (Rel. 01, Created)                                    |                        |
| DT 21-JUL-1986 (Rel. 01, Last sequence update)                       |                        |
| DT 15-JUL-1999 (Rel. 38, Last annotation update)                     |                        |
| DE Ig kappa chain V-III region PC 7183.                              |                        |
| OS Mus musculus (Mouse).   |                        |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                        |

```
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
  "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790(1978).
DR HSP; P01679; KVM583.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Mus musculus (Mouse).
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 3
KV30_MOUSE
ID KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 5308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
  "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790(1978).
DR HSP; P80362; LWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Mus musculus (Mouse).
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 4
KV30_MOUSE
ID KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
  "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSP; P80362; LWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 5
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
  "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RT
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Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 4
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
  "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSP; P80362; LWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYM 15
DB 24 KASQSVYDGDGYM 38
|||||

RESULT 5
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
  "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RT
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Fri Feb 14 15:00:55 2003

us-09-701-001b-4.rsp

RL Nature 276:785-790(1978).  
 DR PIR: D01937; KVM510.  
 DR HSP: P01679; 2FBJ.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 100  
 FT DOMAIN 101 110  
 FT DOMAIN 110 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 96.2%; Score 76; DB 1; Length 110;  
 Best Local Similarity 93.3%; Pred. No. 3.5e-06;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDGYM 15  
 |||||:|||||  
 Db 24 KASQSLDYDGDGYM 38

RESULT 6  
 KV3L\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01664;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region CBPC 101.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.

Query Match 96.1%; Score 68; DB 1; Length 111;  
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;  
 Matches 13; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KASQSDYDGDGYM 15  
 |||||:|||||  
 Db 24 KASQSLDYDGDGYM 38

Query Match 86.1%; Score 68; DB 1; Length 111;  
 Best Local Similarity 86.7%; Pred. No. 8.1e-05;  
 Matches 13; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KASQSDYDGDGYM 15  
 |||||:|||||  
 Db 24 KASQSLDYDGDGYM 38

RESULT 7  
 KV3C\_MOUSE STANDARD; PRT; 111 AA.  
 ID KV3C\_MOUSE  
 AC P01656;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region MOPC 70.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=67056897; PubMed=4162931;  
 RA Gray W.R., Dreyer W.J., Hood L.E.;  
 RT "Mechanism of antibody synthesis: size differences between mouse  
 kappa chains";  
 RL Science 155:465-467(1967).  
 CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
 DR PIR: A01930; KVM580.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Benice-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11904 MW; 4FE7ABC9DF0FC125 CRC64;

Query Match 57.0%; Score 45; DB 1; Length 111;  
 Best Local Similarity 60.0%; Pred. No. 0.66;  
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDGYM 15  
 |||||:|||||  
 Db 24 RASEVDNDSGISEPMN 38

RESULT 8  
 KIF2\_XENLA STANDARD; PRT; 682 AA.  
 ID KIF2\_XENLA  
 AC Q91637;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Kinesin-like protein KIF2 (Kinesin-related protein XKIF2).  
 GN KIF2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND REVISIONS.  
 RX Walczak C.E.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 124-682 FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=96140638; PubMed=8548824;  
 RX Walczak C.E., Mitchison T.J., Desai A.;



RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity";  
RL Nature 276:785-790(1978).  
DR PIR: A01940; KVM54.  
DR HSP: P80362; IWLTL.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 108  
FT DISULFID 23 92  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; D40921D18DAC4B9E CRC64;

Query Match 51.9%; Score 41; DB 1; Length 108;  
Best Local Similarity 60.0%; Pred. No. 3.1;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:||||| :|:|:  
Db 24 RASQSVSTGCGSYMH 38

RESULT 12  
KV3H\_MOUSE STANDARD; PRT; 111 AA.  
AC PV01660;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 3741/TEPC 111.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE (PC 3741).  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity";  
RL Nature 276:785-790(1978).  
RN [2]  
RP SEQUENCE (TEPC 111).  
RX MEDLINE=79012520; PubMed=99744;  
RA McKean D.J., Bell M., Potter M.;  
RT "Mechanisms of antibody diversity: multiple genes encode structurally  
related mouse kappa variable regions";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
DR PIR: A01934; KVM537.  
DR HSP: P01679; 2FBJ.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; D7DF0609303453CE CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;  
Best Local Similarity 53.3%; Pred. No. 3.2;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

FT NON\_TER 111  
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;  
Query Match 51.9%; Score 41; DB 1; Length 111;  
Best Local Similarity 53.3%; Pred. No. 3.2;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:||||| :|:|:  
Db 24 RASQSVSTGCGSYMH 38

RESULT 13  
KV3J\_MOUSE STANDARD; PRT; 111 AA.  
ID KV3J\_MOUSE  
AC P01662;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region ABPC 22/PC 9245.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE (ABPC 22).  
RX MEDLINE=79012520; PubMed=99744;  
RA McKean D.J., Bell M., Potter M.;  
RT "Mechanisms of antibody diversity: multiple genes encode structurally  
related mouse kappa variable regions";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
RN [2]  
RP SEQUENCE (PC 9245).  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity";  
RL Nature 276:785-790(1978).  
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
DR PIR: A01935; KVM56.  
DR HSP: P01679; 2FBJ.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;  
Best Local Similarity 53.3%; Pred. No. 3.2;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDYGDSYMN 15  
:||||| :|:|:  
Db 24 RASQSVSTGCGSYMH 38

RESULT 14  
KV3K\_MOUSE STANDARD; PRT; 111 AA.  
ID KV3K\_MOUSE  
AC P01663;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01935; KVM5M6.
DR HSSP; P01679; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 51.9%; Score 41; DB 1; Length 111;
Best Local Similarity 53.3%; Pred. NO. 3.2;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15
Db 24 RASESVDSYGNSEFMH 38
:||||| i:|:|:

RESULT 15
KV31_MOUSE
ID KV31_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
```

```

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVM5M6.
HSSP; P01679; 2FEJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 51.9%; Score 41; DB 1; Length 131;
Best Local Similarity 53.3%; Pred. NO. 3.8;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMN 15
Db 44 RASESVDSYGNSEFMH 58
:||||| i:|:|:

Search completed: February 14, 2003, 11:16:22
Job time : 8.74194 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 31.2097 Seconds  
(without alignments)  
99.030 Million cell updates/sec

Title: US-09-701-001B-4  
Perfect score: 79  
Sequence: 1 KASQSVYDGD SYMN 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues 671580  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_21.\*
- 1: sp-archaea.\*
  - 2: sp-bacteria.\*
  - 3: sp-fungi.\*
  - 4: sp-human.\*
  - 5: sp-invertebrate.\*
  - 6: sp-mammal.\*
  - 7: sp-mhc.\*
  - 8: sp-organelle.\*
  - 9: sp-phage.\*
  - 10: sp-plant.\*
  - 11: sp-rodent.\*
  - 12: sp-virus.\*
  - 13: sp-vertebrate.\*
  - 14: sp-unclassified.\*
  - 15: sp-rvivirus.\*
  - 16: sp-bacteriap.\*
  - 17: sp-archeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID     | Description        |
|------------|-------|---------------|--------|-----------|--------------------|
| 1          | 48    | 60.8          | 282    | 16 Q8ZKU0 | Q8ZKU0 salmonella  |
| 2          | 48    | 60.8          | 282    | 16 Q8Z2S9 | Q8Z2S9 salmonella  |
| 3          | 44    | 55.7          | 542    | 5 Q9NJD9  | Q9NJD9 onchocerca  |
| 4          | 44    | 55.7          | 815    | 3 Q9C107  | Q9C107 schizosacch |
| 5          | 43    | 54.4          | 137    | 11 P97596 | P97596 rattus norv |
| 6          | 43    | 54.4          | 186    | 5 Q9W2L0  | Q9W2L0 drosophila  |
| 7          | 43    | 54.4          | 551    | 10 P93370 | P93370 nicotiana t |
| 8          | 43    | 54.4          | 1868   | 10 Q9LVX3 | Q9LVX3 polytomella |
| 9          | 42    | 53.2          | 153    | 10 Q9AQY5 | Q9AQY5 mus musculu |
| 10         | 42    | 53.2          | 218    | 11 Q9Z5S1 | Q9Z5S1 mus musculu |
| 11         | 42    | 53.2          | 303    | 16 Q9KA25 | Q9KA25 bacillus ha |
| 12         | 41    | 51.9          | 168    | 11 Q9JI46 | Q9JI46 mus musculu |
| 13         | 41    | 51.9          | 172    | 4 Q95989  | Q95989 homo sapien |
| 14         | 41    | 51.9          | 336    | 2 Q9X6V5  | Q9X6V5 pseudomonas |
| 15         | 41    | 51.9          | 340    | 16 Q9HX24 | Q9HX24 pseudomonas |
| 16         | 40    | 50.6          | 131    | 10 Q9SRP5 | Q9SRP5 arabidopsi  |

|    |    |      |      |           |                    |
|----|----|------|------|-----------|--------------------|
| 17 | 40 | 50.6 | 137  | 10 Q9SRP4 | Q9SRP4 arabidopsi  |
| 18 | 40 | 50.6 | 154  | 17 Q27163 | Q27163 methanobact |
| 19 | 40 | 50.6 | 176  | 3 Q42711  | Q42711 schizosacch |
| 20 | 40 | 50.6 | 180  | 11 Q9D058 | Q9D058 mus musculu |
| 21 | 40 | 50.6 | 197  | 16 Q92L50 | Q92L50 rhizobium m |
| 22 | 40 | 50.6 | 247  | 11 Q9WV63 | Q9WV63 rattus norv |
| 23 | 40 | 50.6 | 311  | 2 Q86071  | Q86071 pseudomonas |
| 24 | 40 | 50.6 | 420  | 10 Q9SIV3 | Q9SIV3 arabidopsi  |
| 25 | 40 | 50.6 | 609  | 4 Q9H2V9  | Q9H2V9 homo sapien |
| 26 | 40 | 50.6 | 610  | 11 Q9D6X1 | Q9D6X1 mus musculu |
| 27 | 40 | 50.6 | 610  | 11 Q99KW9 | Q99KW9 mus musculu |
| 28 | 40 | 50.6 | 610  | 11 Q8R4E1 | Q8R4E1 rattus norv |
| 29 | 40 | 50.6 | 612  | 4 Q8TB96  | Q8TB96 homo sapien |
| 30 | 40 | 50.6 | 615  | 4 Q9BRE2  | Q9BRE2 homo sapien |
| 31 | 40 | 50.6 | 659  | 11 Q54744 | Q54744 mus musculu |
| 32 | 40 | 50.6 | 678  | 11 Q91W03 | Q91W03 mus musculu |
| 33 | 40 | 50.6 | 808  | 10 Q9SW62 | Q9SW62 arabidopsi  |
| 34 | 40 | 50.6 | 921  | 10 Q9FH44 | Q9FH44 arabidopsi  |
| 35 | 40 | 50.6 | 984  | 12 Q8QS29 | Q8QS29 chimpanzee  |
| 36 | 40 | 50.6 | 2439 | 5 Q9VMS2  | Q9VMS2 drosophila  |
| 37 | 39 | 49.4 | 103  | 11 Q9JL80 | Q9JL80 mus musculu |
| 38 | 39 | 49.4 | 196  | 9 Q94MM9  | Q94MM9 cyanophage  |
| 39 | 39 | 49.4 | 200  | 2 Q9AER3  | Q9AER3 serratia ma |
| 40 | 39 | 49.4 | 262  | 5 Q05432  | Q05432 bombyx mori |
| 41 | 39 | 49.4 | 276  | 17 Q9HRR1 | Q9HRR1 halobacteri |
| 42 | 39 | 49.4 | 349  | 10 Q9FNE9 | Q9FNE9 arabidopsi  |
| 43 | 39 | 49.4 | 445  | 2 Q9AMT8  | Q9AMT8 bradyrhizob |
| 44 | 39 | 49.4 | 508  | 5 Q9NA84  | Q9NA84 caenorhabdi |
| 45 | 39 | 49.4 | 509  | 5 Q27482  | Q27482 caenorhabdi |

ALIGNMENTS

RESULT 1

| ID | Q8ZKU0  | PRELIMINARY; | PRT; | 282 AA. |
|----|---|--------------|------|---------|
| AC | Q8ZKU0;   |              |      |         |
| DT | 01-NAR-2002 (TREMREL. 20, Created)  |              |      |         |
| DT | 01-NAR-2002 (TREMREL. 20, Last sequence update)   |              |      |         |
| DT | 01-MAR-2002 (TREMREL. 20, Last annotation update)   |              |      |         |
| DE | Putative cytoplasmic protein.   |              |      |         |
| GN | STM4015.  |              |      |         |
| OS | Salmonella typhimurium.   |              |      |         |
| OC | Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  |              |      |         |
| OC | Salmonella.   |              |      |         |
| OX | NCBI_TaxID=602;   |              |      |         |
| RN | [1]   |              |      |         |
| RP | SEQUENCE FROM N.A.  |              |      |         |
| RC | STRAIN=LT2 / SGSC1412 / ATCC 700720;  |              |      |         |
| RX | MEDLINE=21534948; PubMed=11677609;  |              |      |         |
| RA | McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; |              |      |         |
| RT | *Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.*  |              |      |         |
| RL | Nature 413:852-856(2001).   |              |      |         |
| DR | EMBL: AE008887; AAL22854.1; -.  |              |      |         |
| KW | Hypothetical protein; Complete proteome.  |              |      |         |
| SQ | SEQUENCE 282 AA; 31896 MW; 192CAAE31679D2C6 CRC64;  |              |      |         |

Query Match 60.8%; Score 48; DB 16; Length 282;  
Best Local Similarity 60.0%; Pred. No. 3.1;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSVYDGD SYMN 15

Db 263 EALEPDDYDGD IYMN 277

RESULT 2

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Q822S9
ID Q822S9 PRELIMINARY; PRT; 282 AA.
AC Q822S9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical protein STY3863.
GN STY3863.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OC NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627279; CAP09611.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 282 AA; 31930 MW; EBCB0B08D8D6E877 CRC64;

Query Match 60.8%; Score 48; DB 16; Length 282;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQVDYDGDYSYN 15
Db 263 EALEPDDYDGDYNN 277
I:| | | | | | | | | |

RESULT 3
Q9NJD9 PRELIMINARY; PRT; 542 AA.
ID Q9NJD9;
AC Q9NJD9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Calcium-binding protein CBP-1.
GN CBP-1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20278137; PubMed=10816503;
RA Lizotte-Waniewski M., Tawe W., Gulliano D.B., Lu W., Liu J.,
RA Williams S.A., Lustigman S.;
RT "Identification of potential vaccine and drug target candidates by
RT expressed sequence tag analysis and immunoscreening of Onchocerca
RT volvulus larval cDNA libraries."
RL Infect. Immun. 68:3491-3501(2000).
DR EMBL; AF153720; AAF64251.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 10.
DR SMART; SM00034; EFh; 8.
DR PROSITE; PS00018; EF_HAND;
SQ SEQUENCE 542 AA; 61269 MW; 94E3D57FB72D805B CRC64;

Query Match 55.7%; Score 44; DB 5; Length 542;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 4 QSDYDGDYSYN 15
Db 380 QEIDSDGDYIN 391
I:| | | | | | | | | |

RESULT 4
Q9CL07 PRELIMINARY; PRT; 815 AA.
ID Q9CL07;
AC Q9CL07;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 91.0 kDa protein.
GN SPAPBIE7.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AL590605; CAC36919.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 815 AA; 90985 MW; D3AD3EF2D7997C54 CRC64;

Query Match 55.7%; Score 44; DB 3; Length 815;
Best Local Similarity 80.0%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SVDYDGDYSYN 14
Db 366 SLDLDGDYSYN 375
I:| | | | | | | | | |

RESULT 5
P97596 PRELIMINARY; PRT; 137 AA.
ID P97596;
AC P97596;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Mast cell protease 10 (Fragment).
GN MCP-10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=97149430; PubMed=8996238;
RA Lutzeltschwa C., Pejler G., Aveskogh M., Hellman L.;
RT "Secretory granule proteases in rat mast cells. Cloning of 10
RT different serine proteases and a carboxypeptidase A from various rat
RT mast cell populations."
RL J. Exp. Med. 185:13-29(1997).
DR EMBL; U67913; AAB48266.1; -.
DR HSP; P04187; 2CPI.
DR MEROPS; S01.008; -.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; TRYP-SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.

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FT NON\_TER 1 1  
FT NON\_TER 137 137  
SQ SEQUENCE 137 AA; 83632B52786085BF CRC64;  
Query Match 54.4%; Score 43; DB 11; Length 137;  
Best Local Similarity 53.3%; Pred. No. 10;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 KASQSDYDGDSDSYM 15  
DB 29 KAKPHENYDGDSDHFN 43  
RESULT 6  
ID Q9W2L0 PRELIMINARY; PRT; 186 AA.  
AC Q9W2L0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE CG9406 protein.  
GN CG9406.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman K.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington G., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou W., Zhou S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003453; AA46680.1;  
DR HSP; F02588; 1F0N.  
DR FlyBase; FBgn0034592; CG9406.  
DR InterPro; IPR002048; EF-hand.

DR Pfam: PF00036; efhand; 2.  
DR ProDom: PD000012; EP-hand; 1.  
SQ SEQUENCE 186 AA; 21301 MW; 7B8A6AA5A87AFAFE CRC64;  
Query Match 54.4%; Score 43; DB 5; Length 186;  
Best Local Similarity 50.0%; Pred. No. 14;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KASQSDYDGDSDSYM 14  
DB 56 KATSDVDYDGPGEAHL 69  
RESULT 7  
ID P93370 PRELIMINARY; PRT; 551 AA.  
AC P93370;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Calmodulin-binding protein.  
GN TCB60.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WISCONSIN 38;  
RT Dash S., Lu Y., Harrington H.M.;  
RT "Molecular cloning and characterization of a tobacco calmodulin-  
RT binding protein.";  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U58971; AAB37246.1;  
SQ SEQUENCE 551 AA; 61598 MW; 813879E25125C374 CRC64;  
Query Match 54.4%; Score 43; DB 10; Length 551;  
Best Local Similarity 53.8%; Pred. No. 49;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 3 SQSDVDYDGDSDSYM 15  
DB 292 NQVVEYDGRKSFNL 304  
RESULT 8  
ID Q9LVX3 PRELIMINARY; PRT; 1868 AA.  
AC Q9LVX3;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Genomic DNA, chromosome 3, pl clone; MGF10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=COLUMBIA;  
RX MEDLINE=20277480; PubMed=10819329;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
RT features of the regions of 4,504,864 bp covered by sixty pl and TAC  
RT clones.";  
RL DNA Res. 7:131-135(2000).

```

DR EMBL; AB018114; BAB02691.1; -.
DR InterPro; IPR001395; ALdo/ket.red.
DR PROSITE; PS00063; ALDOKEETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 1868 AA; 206712 MW; 0799ADC38CC0C5F0 CRC64;

Query Match          54.4%; Score 43; DB 10; Length 1868;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSVVDGDSYMN 15
Db 1074 EASASDSDSYRN 1088

RESULT 9
ID Q9AQY5 PRELIMINARY; PRT; 153 AA.
AC Q9AQY5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome C oxidase polypeptide II (EC 1.9.3.1).
GN COX2B
OS Polytomella sp. 'Pringsheim 198.80'.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Polytomella.
OX NCBI_TaxID=37502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRINGSHEIM 198.80;
RX PubMed=11094061;
RA Perez-Martinez X., Antaramian A., Vazquez-Acevedo M., Funes S.,
RA Tolkunova E., d'Alayer J., Claros M.G., Davidson E., King M.P.,
RA Gonzalez-Halphen D.;
RT "Subunit II of Cytochrome C Oxidase in Chlamydomonas Algae Is a
RT Heterodimer Encoded by Two Independent Nuclear Genes.";
RL J. Biol. Chem. 276:11302-11309(2001).
CC 1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2
CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER
CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY
CC SIMILARITY).
CC 1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICCYTOCHROME
CC C + 2 H(2)O.
CC 1- COFACTOR: COPPER A AND HEME GROUP (BY SIMILARITY).
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
EMBL; AF305542; AAK32116.1; -.
DR EMBL; AF305079; AAK30366.1; -.
DR HSSP; F18400; ICYX.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CuA; 1.
DR PROSITE; PS00078; COX2; 1.
KW Copper; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
SQ SEQUENCE 153 AA; 17219 MW; A69030F3E4746238 CRC64;

Query Match          53.2%; Score 42; DB 10; Length 153;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASQSVVDGDSYMN 14
Db 36 ASQPIQYFNDSYMN 48

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RESULT 10
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

Query Match          53.2%; Score 42; DB 11; Length 218;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KASQSVVDGDSYMN 15
Db 159 RASEVDNIGISFMN 173

RESULT 11
Q9KA25 PRELIMINARY; PRT; 303 AA.
ID Q9KA25
AC Q9KA25;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Integrase/recombinase.
GN CODY OR BK2465.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001515; BAB06184.1; -.
DR HSSP; P21891; LAOP.
DR InterPro; IPR002104; Phage_integrase.
DR InterPro; IPR004107; Phage_integr_N.
DR Pfam; PF00589; Phage_integrase; 1.
DR Pfam; PF02899; Phage_integr_N; 1.

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Fri Feb 14 15:00:56 2003

us-09-701-001b-4.rspt

KW Complete proteome.  
SQ SEQUENCE 303 AA; 35035 MW; D10E8A8AFE1D6705 CRC64;  
Query Match 53.2%; Score 42; DB 16; Length 303;  
Best Local Similarity 53.3%; Pred. No. 37;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 KASQSVYDGDGY 15  
DB 204 KKSQSVLDPLFLN 218  
RESULT 12  
Q9JI46 PRELIMINARY; PRT; 168 AA.  
AC Q9JI46  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-JUN-2000 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2000 (Tremblrel. 21, Last annotation update)  
DE Diphosphoinositol polyphosphate phosphohydrolase (Nudix (nucleotide  
diphosphate linked moiety X)-type motif 3).  
GN NUDT3 OR DIPP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RA Chu C., Timo K., Lisanti M., Burstein D., Kohtz D.;  
RT "Ectopic Expression of Diphosphoinositol Polyphosphate  
Phosphohydrolase (DIPP).";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF264064; AAF74761.1; -;  
DR EMBL; BC016534; AAH16534.1; -;  
DR MGD; MGI:1928484; Nudt3.  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
DR PRINTS; PR00502; NUDIXFAMILY.  
DR PROSITE; PS00893; NUDIX; UNKNOWN\_1.  
KW Hydrolase. 168 AA; 19029 MW; E543BE5CE520910 CRC64;  
SQ SEQUENCE 168 AA; 19029 MW; E543BE5CE520910 CRC64;  
Query Match 51.9%; Score 41; DB 11; Length 168;  
Best Local Similarity 53.8%; Pred. No. 28;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 KASQSVYDGDGY 13  
DB 5 KSNQTRTYDGDGY 17  
RESULT 13  
Q95989 PRELIMINARY; PRT; 172 AA.  
ID Q95989  
AC Q95989;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE DIPHOSPHOINOSITOL polyphosphate phosphohydrolase (NUDIX (Nucleoside  
diphosphate linked moiety X)-type motif 3).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RX MEDLINE=99043866; PubMed=9822604;

SAfrany S.T., Caffrey J.J., Yang X., Bembenek M.E., Moyer M.B.,  
Burkhardt W.A., Shears S.B.;  
RT "A novel context for the 'Nutr' module, a guardian of cell integrity,  
in a diphosphoinositol polyphosphate phosphohydrolase.";  
RL EMBO J. 17:6599-6607(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA Strausberg R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF062530; AAC83225.1; -;  
DR EMBL; AF062529; AAC83224.1; -;  
DR EMBL; BC007727; AAH07727.1; -;  
DR InterPro; IPR000086; NUDIX\_hydrolase.  
DR Pfam; PF00293; NUDIX; 1.  
DR PRINTS; PR00502; NUDIXFAMILY.  
DR PROSITE; PS00893; NUDIX; UNKNOWN\_1.  
KW Hydrolase. 172 AA; 19471 MW; DE823FECF5C6438A CRC64;  
SQ SEQUENCE 172 AA; 19471 MW; DE823FECF5C6438A CRC64;  
Query Match 51.9%; Score 41; DB 4; Length 172;  
Best Local Similarity 53.8%; Pred. No. 29;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 KASQSVYDGDGY 13  
DB 5 KSNQTRTYDGDGY 17  
RESULT 14  
Q9X6V5 PRELIMINARY; PRT; 336 AA.  
ID Q9X6V5  
AC Q9X6V5;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
DE Membrane-bound lytic transglycosylase precursor.  
GN MLTB.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PA01;  
RA Gagnon L.A.; Castro-Urbina I.M., Liao X., Hancock R.E.W., Clarke A.J.,  
RA Huletsky A.;  
RT "Cloning and characterization of PBP5 of Pseudomonas aeruginosa.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF147448; AAD32232.1; -;  
DR HSSP; P41052; ILTM.  
KW Signal.  
FT SIGNAL 1 29 POTENTIAL.  
FT SIGNAL 336 336 POTENTIAL.  
SQ SEQUENCE 336 AA; 37423 MW; 1DAFBE8991787BBE CRC64;  
Query Match 51.9%; Score 41; DB 2; Length 336;  
Best Local Similarity 54.5%; Pred. No. 62;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 5 SVDYDGDGY 15  
DB 204 AVDFDGDGHIN 214  
RESULT 15  
Q9HX24 PRELIMINARY; PRT; 340 AA.  
ID Q9HX24  
AC Q9HX24;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Membrane-bound lytic transglycosylase.

Search completed: February 14, 2003, 11:18:41  
Job time : 33.3763 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 18.9677 Seconds  
(without alignments)  
49.176 Million cell updates/sec

Title: US-09-701-001B-5  
Perfect score: 31  
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | ID      | Description            |
|------------|-------------|-------|--------|---------|------------------------|
| 1          | 31          | 100.0 | 7      | AA70196 | Mab 3B9 light chain    |
| 2          | 31          | 100.0 | 7      | AA70196 | Anti-Fas Mab HFE7A     |
| 3          | 31          | 100.0 | 7      | AA70196 | CDR of the light chain |
| 4          | 31          | 100.0 | 7      | AA70196 | Light chain CDR fo     |
| 5          | 31          | 100.0 | 7      | AA70196 | Mouse anti-Fas ant     |
| 6          | 31          | 100.0 | 7      | AA70196 | Murine anti-Fas an     |
| 7          | 31          | 100.0 | 7      | AA70196 | Antibody 4H5 L cha     |
| 8          | 31          | 100.0 | 7      | AA70196 | Murine CD4/CD34 re     |
| 9          | 31          | 100.0 | 7      | AA70196 | Mouse AC10 antibod     |
| 10         | 31          | 100.0 | 7      | AA70196 | Humanised anti-Fas     |

|    |    |       |     |          |                     |
|----|----|-------|-----|----------|---------------------|
| 11 | 31 | 100.0 | 7   | ABB74910 | Humanised anti-Fas  |
| 12 | 31 | 100.0 | 7   | AAU70353 | Mouse Kappa III li  |
| 13 | 31 | 100.0 | 15  | AAU70353 | CD-4 antibody varia |
| 14 | 31 | 100.0 | 41  | AAU70353 | IF7 antibody varia  |
| 15 | 31 | 100.0 | 103 | AAU70353 | Antibody 4H5 L cha  |
| 16 | 31 | 100.0 | 103 | AAU70353 | Murine derived pro  |
| 17 | 31 | 100.0 | 106 | AAU70353 | MaE15 light chain   |
| 18 | 31 | 100.0 | 106 | AAU70353 | Light chain amino   |
| 19 | 31 | 100.0 | 111 | AAU70353 | Immunoglobulin L C  |
| 20 | 31 | 100.0 | 111 | AAU70353 | Mouse anti-HIV mu5  |
| 21 | 31 | 100.0 | 111 | AAU70353 | Mouse-human chim    |
| 22 | 31 | 100.0 | 111 | AAU70353 | Anti HIV antibody   |
| 23 | 31 | 100.0 | 111 | AAU70353 | Chimeric anti HIV   |
| 24 | 31 | 100.0 | 111 | AAU70353 | Light chain variab  |
| 25 | 31 | 100.0 | 111 | AAU70353 | Light chain sequen  |
| 26 | 31 | 100.0 | 111 | AAU70353 | Antibody 4H5 L cha  |
| 27 | 31 | 100.0 | 111 | AAU70353 | Murine derived pro  |
| 28 | 31 | 100.0 | 111 | AAU70353 | Mouse AC10 antibod  |
| 29 | 31 | 100.0 | 111 | AAU70353 | Human x mouse modi  |
| 30 | 31 | 100.0 | 112 | AAU70353 | Monoclonal antibod  |
| 31 | 31 | 100.0 | 113 | AAU70353 | Anti-Leu 3a light   |
| 32 | 31 | 100.0 | 115 | AAU70353 | Amino acids sequen  |
| 33 | 31 | 100.0 | 131 | AAU70353 | Anti-Leu 3a light   |
| 34 | 31 | 100.0 | 131 | AAU70353 | Anti-CD4 antibody   |
| 35 | 31 | 100.0 | 131 | AAU70353 | Humanized antibody  |
| 36 | 31 | 100.0 | 131 | AAU70353 | Humanized antibody  |
| 37 | 31 | 100.0 | 131 | AAU70353 | Variable kappa cha  |
| 38 | 31 | 100.0 | 131 | AAU70353 | Light chain variab  |
| 39 | 31 | 100.0 | 131 | AAU70353 | Light chain sequen  |
| 40 | 31 | 100.0 | 131 | AAU70353 | Light chain sequen  |
| 41 | 31 | 100.0 | 131 | AAU70353 | Mouse Mab 3B9 ligh  |
| 42 | 31 | 100.0 | 131 | AAU70353 | Light chain variab  |
| 43 | 31 | 100.0 | 132 | AAU70353 | Light chain sequen  |
| 44 | 31 | 100.0 | 132 | AAU70353 | Mouse Mab 3B9 ligh  |
| 45 | 31 | 100.0 | 132 | AAU70353 | Light chain sequen  |

ALIGNMENTS

RESULT 1  
AA70196  
ID AA70196 standard; Protein; 7 AA.  
XX  
AC AA70196;  
XX  
DT 20-SEP-1995 (first entry)  
XX  
DE Mab 3B9 light chain CDR.  
XX  
Chimeric antibody; humanized antibody; antibody engineering;  
KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;  
KW complementarity determining region.  
XX  
Mus sp.  
OS  
XX  
PN WO9507301-A.  
XX  
PD 16-MAR-1995.  
XX  
PF 07-SEP-1994; 94WO-US10308.  
XX  
PR 07-SEP-1993; 93US-0117366.  
PR 14-OCT-1993; 93US-0136783.  
PR  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PIC.  
XX  
PI Gross MS, Holmes SD, Sylvester DR;  
XX WPI; 1995-123387/16.  
XX  
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived

PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 XX and IgE-mediated allergic conditions

PS Disclosure; Page 55; 97pp; English.

XX Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 MAB secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pGEM7f+ and transformed into E. coli  
 CC DH5-alpha. A light chain cDNA clone was sequenced (AA083490) that  
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were  
 CC identified.

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||||  
 1 AASNLES 7

RESULT 2

ID AAW83028 standard; Peptide; 7 AA.

XX AAW83028;

XX 15-MAR-1999 (first entry)

DE Anti-Fas MAB HFE7A light chain CDR-L2.

XX HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy; complementarity determining region;  
 KW CDR.

XX Mus musculus.

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS

XX Claim 9; Page 185; 292pp; English.

XX

CC This is the amino acid of complementarity determining region 2  
 CC (CDR-L2) of the light chain (see AAW83042) of murine anti-human Fas  
 CC monoclonal antibody HFE7A. The invention relates to antibodies,  
 CC especially humanised antibodies (see AAW83031-37), recognising the  
 CC Fas antigen. Such antibodies preferably comprise a heavy chain and  
 CC a light chain including CDRs (see AAW83024-29) from the heavy and  
 CC light chains of HFE7A. Humanised antibodies are produced by CDR  
 CC grafting. The antibodies are capable of inducing apoptosis in  
 CC abnormal cells expressing Fas, and of inhibiting Fas-induced  
 CC apoptosis in normal cells. They are used to evaluate, in animal  
 CC models, treatments of diseases that involve Fas/Fas ligand  
 CC interactions, and also to treat such diseases, including autoimmune  
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's  
 CC disease, thrombopenia purpura and insulin-dependent diabetes),  
 CC allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and  
 CC transplant rejection (all claimed).

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

|||||

1 AASNLES 7

RESULT 3

AA23773

ID AAY23773 standard; Peptide; 7 AA.

XX AAY23773;

XX 13-SEP-1999 (first entry)

DE CDR of the light chain variable region of antibody 3B9.

XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;  
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
 KW allergy; complementarity determining region.

XX Mus sp.

XX US5928904-A.

XX 27-JUL-1999.

XX 07-JUN-1995; 95US-0483632.

XX 07-JUN-1995; 95US-0483632.

XX 07-SEP-1993; 93US-0117366.

XX 14-OCT-1993; 93US-0136783.

XX 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Gross MS, Holmes SD, Sylvester DR;

XX WPI; 1999-429500/36.

XX N-PSDB; AAX85890.

XX New DNA molecules encoding recombinant antibodies useful for  
 PT treating IL4-mediated conditions

XX PS Example 3; Column 43-44; 50pp; English.

XX CC The present sequence represents a complementarity determining region (CDR) of the light chain variable region of murine interleukin-4 (IL-4) antibody 3B9. The specification describes chimeric and humanised IL-4 monoclonal antibodies. The antibodies of the invention are used in therapeutic and pharmaceutical compositions for treating IL-4 mediated and immunoglobulin E-mediated allergic reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis, atopic asthma, anaphylactic shock, rheumatoid arthritis, host-versus-graft disease and renal disease. They are also useful in the diagnosis of an allergy or condition associated with excess IL-4 production through the measurement e.g. by ELISA of circulating endogenous IL-4 levels in humans.

XX CC Sequence 7 AA;

XX CC Query Match 100.0%; Score 31; DB 20; Length 7;

XX CC Best Local Similarity 100.0%; Pred. No. 7.8e+05;

XX CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC

XX CC 1 AASNLES 7

XX CC |||||

XX CC 1 AASNLES 7

XX CC

XX CC RESULT 4

XX CC AAY18115

XX CC ID AAY18115 standard; peptide; 7 AA.

XX CC AC AAY18115;

XX CC DT 11-AUG-1999 (first entry)

XX CC

XX CC Light chain CDR for hIL-4 specific antibody.

XX CC Antibody: interleukin-4; IL4; immunoglobulin E; IgE mediated disease;

XX CC allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;

XX CC atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;

XX CC autoimmune disease; graft versus host disease;

XX CC complementarity determining region; CDR.

XX CC Synthetic.

XX CC US5914110-A.

XX CC 22-JUN-1999.

XX CC 07-JUN-1995; 95US-0483636.

XX CC 07-JUN-1995; 95US-0483636.

XX CC 07-SEP-1993; 93US-0117366.

XX CC 14-OCT-1993; 93US-0136783.

XX CC 07-SEP-1994; 94WO-US10308.

XX CC (SMIK ) SMITHKLINE BEECHAM CORP.

XX CC (SMIK ) SMITHKLINE BEECHAM PLC.

XX CC Gross MS, Holmes SD, Sylvester DR;

XX CC WPI; 1999-370482/31.

XX CC N-PSDB; AAX79514.

XX CC Recombinant IL4 antibodies

XX CC Claim 7; Column 43; 50pp; English.

XX CC

XX CC This sequence represents a light chain complementarity determining region (CDR) from an antibody of the invention. The antibody is a chimeric or humanised interleukin-4 (IL4) monoclonal antibody for the treatment of immunoglobulin E (IgE) mediated diseases. The antibodies are useful for the treatment of allergic disorders such as allergic rhinitis,

XX CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.

XX CC The antibodies are also useful for regulating B and T cell proliferation and as such are useful in the treatment of autoimmune diseases and graft versus host disease.

XX CC

XX CC Sequence 7 AA;

XX CC Query Match 100.0%; Score 31; DB 20; Length 7;

XX CC Best Local Similarity 100.0%; Pred. No. 7.8e+05;

XX CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX CC

XX CC 1 AASNLES 7

XX CC |||||

XX CC 1 AASNLES 7

XX CC

XX CC RESULT 5

XX CC AAB14745

XX CC ID AAB14745 standard; peptide; 7 AA.

XX CC AC AAB14745;

XX CC DT 24-NOV-2000 (first entry)

XX CC

XX CC Mouse anti-Fas antibody HFE7A light chain CDR2.

XX CC Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

XX CC murine; complementarity determining region; CDR; human Fas;

XX CC Fas ligand; apoptosis modulator; programmed cell death;

XX CC autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;

XX CC cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;

XX CC hepatitis; AIDS; graft rejection; light chain.

XX CC OS Mus musculus.

XX CC JP2000169393-A.

XX CC 20-JUN-2000.

XX CC 30-SEP-1999; 99JP-0278301.

XX CC 30-SEP-1998; 98JP-0276883.

XX CC (SANY ) SANKYO CO LTD.

XX CC WPI; 2000-485645/43.

XX CC Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -

XX CC Claim 10; Page 65; 139pp; Japanese.

XX CC The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14744-B14746 represent CDRs 1-3 of the light chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828).

XX CC

XX CC Sequence 7 AA;

XX CC Query Match 100.0%; Score 31; DB 21; Length 7;

XX CC Best Local Similarity 100.0%; Pred. No. 7.8e+05;

XX CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 Db 1 AASNLES 7

RESULT 6  
 AAW90895  
 ID AAW90895 standard; peptide; 7 AA.  
 AC AAW90895;  
 XX  
 DT 08-AUG-2000 (first entry)  
 DE Murine anti-Fas antibody peptide fragment #5.  
 DE XX.  
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Mus musculus.  
 XX  
 PN EP90663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI; 2000-258930/23.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 PT Disclosure; Page 98; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a murine anti-Fas antibody peptide fragment described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 31; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AASNLES 7  
 Db 1 AASNLES 7

RESULT 7  
 AAY59260  
 ID AAY59260 standard; peptide; 7 AA.  
 AC AAY59260;  
 XX  
 DT 17-APR-2000 (first entry)  
 DE Antibody 4H5 L chain variable region CDR2 fragment.  
 DE XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;  
 KW complementarity determining region.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX  
 PA (ASAH ) ASAMI KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 XX  
 PT An antibody and the nucleic acid coding the antibody -  
 XX  
 PS Claim 2; Page 14; 25pp; Japanese.  
 XX  
 XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. Sequences  
 CC AAY59259-61 represent the complementarity determining region (CDR)-1,  
 CC CDR-2 and CDR-3 fragments in the L chain variable region of the  
 CC antibody 4H5 respectively.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 31; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AASNLES 7  
 Db 1 AASNLES 7

RESULT 8  
 AAY51137  
 ID AAY51137 standard; Protein; 7 AA.  
 XX  
 AC AAY51137;  
 XX  
 DT 31-MAR-2000 (first entry)

XX DE Murine CD4/CD34 recognizing antibody light chain CDR-2 region #1.  
 XX DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 XX KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 XX KW HIV infection; autoimmune disease; complementarity determining region;  
 XX KW CDR-2; light chain; murine.  
 XX OS Mus sp.  
 XX PN WO9961629-A1.  
 XX PD 02-DEC-1999.  
 XX XX 24-MAY-1999; 99WO-JP02711.  
 XX PF 25-MAY-1998; 98JP-0159957.  
 XX PR 26-MAY-1998; 98JP-0163023.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX (ASAH ) ASAH MEDICAL CO LTD.  
 XX Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI; 2000-086720/07.  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 XX the separation of CD4 or CD34 positive cells -  
 XX Claim 3; Page 77; 111pp; Japanese.  
 XX This invention describes a novel device (I) for separating cluster  
 XX differentiation (CD)-positive cells using a recombinant (chimeric or  
 XX single-chain) antibody recognising CD4 or CD34. The devices are useful  
 XX for the separation of CD4 or CD34 positive cells, which is useful for  
 XX the collection of hematopoietic undifferentiated cells, elimination of  
 XX lymphocytes from cells to be used in bone marrow transplantation, the  
 XX detection of leukemic cells and the production of medicinal  
 XX compositions for the treatment of HIV infection and autoimmune diseases.  
 XX This sequence represents a murine derived complementarity determining  
 XX region CDR-2 protein fragment which is used to illustrate the method of  
 XX the invention.  
 XX XX Sequence 7 AA;  
 XX Query Match 100.0%; Score 31; DB 21; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 AASNLES 7  
 XX Db | | | | | | |  
 XX 1 AASNLES 7  
 XX RESULT 9  
 XX AAU99854  
 XX ID AAU99854 standard; Peptide; 7 AA.  
 XX AC AAU99854;  
 XX DT 07-OCT-2002 (first entry)  
 XX DE Mouse AC10 antibody light chain CDR2 (L2).  
 XX XX Gene therapy; vaccine; CD30 binding; cytostatic; cytotoxic;  
 XX KW Hodgkin's Disease; mouse; AC10 antibody; light chain CDR;  
 XX KW complementarity determining region.  
 XX XX Mus musculus.  
 XX OS WO200243661-A2.  
 XX PN 06-JUN-2002.  
 XX PD

XX 28-NOV-2001; 2001WO-US44811.  
 XX 28-NOV-2000; 2000US-0724406.  
 XX (SEAT-) SEATTLE GENETICS INC.  
 XX Francisco JA, Risdon G, Wahl AF, Siegall CB;  
 XX WPI; 2002-557522/59.  
 XX N-PSDB; ABK88126.  
 XX Novel antibody that immunospecifically binds to CD30, useful for  
 XX treating Hodgkin's disease, exerts a cytostatic or cytotoxic effect on  
 XX Hodgkin's Disease cell line, and is not monoclonal antibody AC10 or  
 XX Hefi-1 -  
 XX Claim 9; Page 99; 103pp; English.  
 XX The invention describes an antibody (I) that immunospecifically binds to  
 XX CD30, exerts a cytostatic or cytotoxic effect on Hodgkin's Disease cell  
 XX line, and is not monoclonal antibody AC10 or Hefi-1 and does not result  
 XX from cleavage of AC10 or Hefi-1 with papain or pepsin. (I), a protein  
 XX (II) that competes for CD30 binding with the monoclonal antibodies AC10  
 XX or Hefi, or exerts a cytotoxic or cytostatic effect on a Hodgkins'  
 XX disease cell line and the nucleic acid encoding the protein (III) are  
 XX useful for the treatment or prevention of Hodgkin's Disease in a subject,  
 XX by administering (I) to the subject, in the absence of conjugation to a  
 XX cytostatic or cytotoxic agent, respectively and a pharmaceutically  
 XX acceptable carrier. This is the amino acid sequence of the mouse AC10  
 XX antibody light chain complementarity determining region 2 (CDR2), a  
 XX polypeptide that competes with AC10 for CD30 binding.  
 XX XX Sequence 7 AA;  
 XX Query Match 100.0%; Score 31; DB 23; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 AASNLES 7  
 XX Db | | | | | | |  
 XX 1 AASNLES 7  
 XX RESULT 10  
 XX ABB74864  
 XX ID ABB74864 standard; Peptide; 7 AA.  
 XX AC ABB74864;  
 XX DT 26-APR-2002 (first entry)  
 XX DE Humanised anti-Fas antibody related peptide SEQ ID NO 30.  
 XX XX Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;  
 XX KW light chain subunit; apoptosis; immunosuppressive; antiallergic;  
 XX KW autoimmune disease; allergy; atopic.  
 XX OS Homo sapiens.  
 XX XX JP2001342148-A.  
 XX PN 11-DEC-2001.  
 XX PD 28-MAR-2001; 2001JP-0093106.  
 XX XX 29-MAR-2000; 2000JP-0090918.  
 XX PR (SANY ) SANKYO CO LTD.  
 XX XX WPI; 2002-145113/19.  
 XX DR Drug containing humanised anti-Fas antibody, used for preventing and  
 XX PT

PT treating autoimmune diseases, allergy, and atopy -  
 PS Example 6 (Preparatory); Page 26; 194pp; Japanese.

XX The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in Fas/Fas ligand system containing as the active  
 CC component an antibody having as the light chain subunit a polypeptide  
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,  
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all  
 CC fully defined in the specification and having an activity of combining  
 CC specifically with mammalian Fas and an activity of inducing apoptosis  
 CC in a cell expressing Fas. The agent has immunosuppressive and  
 CC antiallergic activity and is used for preventing and treating autoimmune  
 CC diseases, allergy, atopy and others. The present sequence is that of a  
 CC peptide, useful to the invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 31; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 1 AASNLES 7

RESULT 11

ABB74910  
 ID ABB74910 standard; Peptide; 7 AA.

AC ABB74910;

XX 30-APR-2002 (first entry)

XX Humanised anti-Fas antibody related peptide SEQ ID NO 27.

XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;  
 KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;  
 KW autoimmune disease; allergy; atopy.

XX Homo sapiens.

XX JP2001342149-A.

XX 11-DEC-2001.

XX 28-MAR-2001; 2001JP-0093243.

XX 29-MAR-2000; 2000JP-0091144.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2002-145114/19.

XX Drug for preventing or treating e.g. autoimmune disease or allergy,  
 PT comprises humanised anti-Fas antibody -

XX Example 6 (preparatory); Page 26; 154pp; Japanese.

XX The invention relates to a preventive or treating agent for diseases  
 CC caused by abnormality in the Fas/Fas ligand system containing, as the  
 CC active component, an antibody having a light chain subunit and a heavy  
 CC chain subunit and an activity of combining specifically with mammalian  
 CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The  
 CC agent has antiallergic, immunosuppressive and apoptotic activity and is  
 CC used for preventing and treating autoimmune diseases, allergy, atopy and  
 CC others. The present sequence is that of a peptide useful to the  
 CC invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 31; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 1 AASNLES 7

RESULT 12

AAU70353  
 ID AAU70353 standard; Peptide; 7 AA.

XX AC AAU70353;

XX 14-FEB-2002 (first entry)

XX Mouse Kappa III light chain CDR2.

XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;  
 KW complementarity determining region; framework region; IgBP;  
 KW transgenic plant; immunoglobulin binding protein array;  
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

XX Mus musculus.

XX WO200183806-A1.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14349.

XX 02-MAY-2000; 2000US-0563222.

XX (EPIC-) EPICYTE PHARM INC.

XX Hiatt AC, Hein MB;

XX WPI; 2002-055482/07.

XX Preparing immunoglobulin binding protein array in plant cells by  
 PT transforming the cells with different polynucleotides encoding binding  
 PT protein polypeptides specific to ligand, selecting plant cells for  
 PT preparing array -

XX Disclosure; Page 14; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant  
 CC cells), comprising using a library of two different polynucleotides  
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides  
 CC that specifically bind to a ligand or form one or more disulphide bonds  
 CC with polypeptides in transfected cells, to generate an IgBP that  
 CC binds to a ligand, and transformed plant cells are selected, and  
 CC preparing an IgBP array in plant cells. At least one peptide sequence has  
 CC at least 75% sequence identity to a framework region (FR) of a native  
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.  
 CC The method is useful for preparing an immunoglobulin binding protein  
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic  
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)  
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The  
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having  
 CC desired characteristics. The present sequence is a mammalian  
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of  
 CC the invention.

XX Sequence 7 AA;

SQ Query Match 100.0%; Score 31; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 1 AASNLES 7



XX 30-NOV-1994; 94US-0351193.  
PR (IMMP-) IMMIPHERON INC.  
XX  
XX PA Muller S, Kohler H;  
XX PI  
XX XX WPI; 2000-338622/29.  
XX  
XX Variable heavy and light chain regions of murine monoclonal antibody  
PT 1F7, useful for treating HIV infection and AIDS -  
XX  
XX Claim 1; Fig 8; 45pp; English.  
XX  
XX The present invention describes the variable heavy and light chain  
CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to  
CC AAY91016 represent specifically claimed amino acid sequences of the  
CC variable light chain, and AAY91017 to AAY91019 represent specifically  
CC claimed amino acid sequence of the variable heavy chain. The antibodies  
CC are used for treatment of HIV (human immunodeficiency virus) infection  
CC and AIDS (acquired immunodeficiency syndrome). They are also used for  
CC detecting HIV in serum and for stimulating HIV antigen related and  
CC committed B cells to produce broadly reactive and neutralising antibodies  
CC by clonotypic stimulation.  
XX  
XX Sequence 41 AA;  
SQ  
Query Match 100.0%; Score 31; DB 21; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6.4; 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AASNLES 7  
DB 12 AASNLES 18  
IIIIIII  
RESULT 15  
AAY59263  
ID AAY59263 standard; protein; 103 AA.  
XX  
XX AC AAY59263;  
XX  
XX 17-APR-2000 (first entry)  
DT  
XX Antibody 4H5 L chain variable region.  
DE  
XX CD4 antigen; anti-human; antibody; 4H5; drug.  
XX  
XX Mus sp.  
OS  
XX JP11332563-A.  
XX  
XX 07-DEC-1999.  
PD  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX (ASAH ) ASahi KASEI KOGYO KK.  
PA  
XX WPI; 2000-091351/08.  
XX  
XX N-PSDB; AAZ59662.  
XX  
XX An antibody and the nucleic acid coding the antibody -  
PT  
XX Claim 5; Page 15-16; 25pp; Japanese.  
PS  
XX The invention provides an antibody having affinity to CD4 antigen. The  
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents the L chain variable region of the antibody 4H5.  
XX  
XX Sequence 103 AA;  
SQ

XX 30-NOV-1994; 94US-0351193.  
PR (IMMP-) IMMIPHERON INC.  
XX  
XX PA Muller S, Kohler H;  
XX PI  
XX XX WPI; 2000-338622/29.  
XX  
XX Variable heavy and light chain regions of murine monoclonal antibody  
PT 1F7, useful for treating HIV infection and AIDS -  
XX  
XX Claim 1; Fig 8; 45pp; English.  
XX  
XX The present invention describes the variable heavy and light chain  
CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to  
CC AAY91016 represent specifically claimed amino acid sequences of the  
CC variable light chain, and AAY91017 to AAY91019 represent specifically  
CC claimed amino acid sequence of the variable heavy chain. The antibodies  
CC are used for treatment of HIV (human immunodeficiency virus) infection  
CC and AIDS (acquired immunodeficiency syndrome). They are also used for  
CC detecting HIV in serum and for stimulating HIV antigen related and  
CC committed B cells to produce broadly reactive and neutralising antibodies  
CC by clonotypic stimulation.  
XX  
XX Sequence 41 AA;  
SQ  
Query Match 100.0%; Score 31; DB 21; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6.4; 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AASNLES 7  
DB 12 AASNLES 18  
IIIIIII  
RESULT 15  
AAY59263  
ID AAY59263 standard; protein; 103 AA.  
XX  
XX AC AAY59263;  
XX  
XX 17-APR-2000 (first entry)  
DT  
XX Antibody 4H5 L chain variable region.  
DE  
XX CD4 antigen; anti-human; antibody; 4H5; drug.  
XX  
XX Mus sp.  
OS  
XX JP11332563-A.  
XX  
XX 07-DEC-1999.  
PD  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX (ASAH ) ASahi KASEI KOGYO KK.  
PA  
XX WPI; 2000-091351/08.  
XX  
XX N-PSDB; AAZ59662.  
XX  
XX An antibody and the nucleic acid coding the antibody -  
PT  
XX Claim 5; Page 15-16; 25pp; Japanese.  
PS  
XX The invention provides an antibody having affinity to CD4 antigen. The  
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents the L chain variable region of the antibody 4H5.  
XX  
XX Sequence 103 AA;  
SQ

XX 30-NOV-1994; 94US-0351193.  
PR (IMMP-) IMMIPHERON INC.  
XX  
XX PA Muller S, Kohler H;  
XX PI  
XX XX WPI; 2000-338622/29.  
XX  
XX Variable heavy and light chain regions of murine monoclonal antibody  
PT 1F7, useful for treating HIV infection and AIDS -  
XX  
XX Claim 1; Fig 8; 45pp; English.  
XX  
XX The present invention describes the variable heavy and light chain  
CC regions (I) of murine monoclonal antibody (mAb) 1F7. AAY91014 to  
CC AAY91016 represent specifically claimed amino acid sequences of the  
CC variable light chain, and AAY91017 to AAY91019 represent specifically  
CC claimed amino acid sequence of the variable heavy chain. The antibodies  
CC are used for treatment of HIV (human immunodeficiency virus) infection  
CC and AIDS (acquired immunodeficiency syndrome). They are also used for  
CC detecting HIV in serum and for stimulating HIV antigen related and  
CC committed B cells to produce broadly reactive and neutralising antibodies  
CC by clonotypic stimulation.  
XX  
XX Sequence 41 AA;  
SQ  
Query Match 100.0%; Score 31; DB 21; Length 41;  
Best Local Similarity 100.0%; Pred. No. 6.4; 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AASNLES 7  
DB 12 AASNLES 18  
IIIIIII  
RESULT 15  
AAY59263  
ID AAY59263 standard; protein; 103 AA.  
XX  
XX AC AAY59263;  
XX  
XX 17-APR-2000 (first entry)  
DT  
XX Antibody 4H5 L chain variable region.  
DE  
XX CD4 antigen; anti-human; antibody; 4H5; drug.  
XX  
XX Mus sp.  
OS  
XX JP11332563-A.  
XX  
XX 07-DEC-1999.  
PD  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX (ASAH ) ASahi KASEI KOGYO KK.  
PA  
XX WPI; 2000-091351/08.  
XX  
XX N-PSDB; AAZ59662.  
XX  
XX An antibody and the nucleic acid coding the antibody -  
PT  
XX Claim 5; Page 15-16; 25pp; Japanese.  
PS  
XX The invention provides an antibody having affinity to CD4 antigen. The  
XX anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents the L chain variable region of the antibody 4H5.  
XX  
XX Sequence 103 AA;  
SQ

Query Match 100.0%; Score 31; DB 21; Length 103;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
| | | | |  
Db 46 AASNLES 52

Search completed: February 14, 2003, 11:15:45  
Job time : 19.9677 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 ; Search time 6.32258 Seconds  
(without alignments)  
32.575 Million cell updates/sec

Title: US-09-701-001B-5  
Perfect score: 31  
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues  
Local number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description        |
|------------|-------|-------|--------|-------|--------------------|
| 1          | 31    | 100.0 | 7      | 2     | US-08-483-636-18   |
| 2          | 31    | 100.0 | 7      | 2     | US-08-483-632-18   |
| 3          | 31    | 100.0 | 41     | 3     | US-08-984-277-6    |
| 4          | 31    | 100.0 | 106    | 3     | US-08-466-151-6    |
| 5          | 31    | 100.0 | 106    | 4     | US-08-466-163B-6   |
| 6          | 31    | 100.0 | 111    | 1     | US-08-491-845-8    |
| 7          | 31    | 100.0 | 111    | 1     | US-08-491-845-16   |
| 8          | 31    | 100.0 | 111    | 2     | US-08-483-636-73   |
| 9          | 31    | 100.0 | 111    | 2     | US-08-483-632-73   |
| 10         | 31    | 100.0 | 115    | 3     | US-08-513-968-51   |
| 11         | 31    | 100.0 | 131    | 2     | US-08-483-636-14   |
| 12         | 31    | 100.0 | 131    | 2     | US-08-483-636-58   |
| 13         | 31    | 100.0 | 131    | 2     | US-08-483-632-14   |
| 14         | 31    | 100.0 | 131    | 2     | US-08-483-632-58   |
| 15         | 31    | 100.0 | 131    | 3     | US-08-589-939-3    |
| 16         | 31    | 100.0 | 131    | 4     | US-08-579-378A-14  |
| 17         | 31    | 100.0 | 131    | 4     | US-08-579-378A-18  |
| 18         | 31    | 100.0 | 132    | 2     | US-08-483-636-2    |
| 19         | 31    | 100.0 | 132    | 2     | US-08-483-632-2    |
| 20         | 31    | 100.0 | 218    | 5     | PCT-US96-13152-2   |
| 21         | 28    | 90.3  | 7      | 2     | US-08-650-262-11   |
| 22         | 28    | 90.3  | 98     | 3     | US-08-881-037-75   |
| 23         | 28    | 90.3  | 108    | 2     | US-08-650-262-2    |
| 24         | 28    | 90.3  | 120    | 1     | US-08-111-080-24   |
| 25         | 28    | 90.3  | 120    | 1     | US-08-211-980-24   |
| 26         | 28    | 90.3  | 120    | 5     | PCT-US93-07967-24  |
| 27         | 27    | 87.1  | 6      | 1     | US-08-137-117D-137 |

|    |    |      |     |   |                   |                    |
|----|----|------|-----|---|-------------------|--------------------|
| 28 | 27 | 87.1 | 6   | 2 | US-08-436-717-137 | Sequence 137, Appl |
| 29 | 27 | 87.1 | 7   | 4 | US-09-425-638A-70 | Sequence 70, Appl  |
| 30 | 27 | 87.1 | 7   | 4 | US-09-543-004-70  | Sequence 70, Appl  |
| 31 | 27 | 87.1 | 17  | 2 | US-08-712-212-5   | Sequence 5, Appli  |
| 32 | 27 | 87.1 | 17  | 5 | PCT-US95-05160-5  | Sequence 5, Appli  |
| 33 | 27 | 87.1 | 20  | 4 | US-09-556-605-19  | Sequence 19, Appl  |
| 34 | 27 | 87.1 | 20  | 4 | US-09-556-605-20  | Sequence 20, Appl  |
| 35 | 27 | 87.1 | 64  | 2 | US-08-765-179B-10 | Sequence 10, Appl  |
| 36 | 27 | 87.1 | 106 | 1 | US-08-202-047-26  | Sequence 26, Appl  |
| 37 | 27 | 87.1 | 106 | 3 | US-08-964-690-26  | Sequence 3, Appli  |
| 38 | 27 | 87.1 | 109 | 4 | US-09-157-370-3   | Sequence 20, Appl  |
| 39 | 27 | 87.1 | 109 | 4 | US-09-425-638A-20 | Sequence 21, Appl  |
| 40 | 27 | 87.1 | 109 | 4 | US-09-425-638A-21 | Sequence 39, Appl  |
| 41 | 27 | 87.1 | 109 | 4 | US-09-425-638A-39 | Sequence 40, Appl  |
| 42 | 27 | 87.1 | 109 | 4 | US-09-425-638A-40 | Sequence 41, Appl  |
| 43 | 27 | 87.1 | 109 | 4 | US-09-425-638A-41 | Sequence 42, Appl  |
| 44 | 27 | 87.1 | 109 | 4 | US-09-425-638A-42 | Sequence 42, Appl  |
| 45 | 27 | 87.1 | 109 | 4 | US-09-425-638A-43 | Sequence 43, Appl  |

ALIGNMENTS

RESULT 1  
US-08-483-636-18  
; Sequence 18, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-483-636-18

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
| | | | |  
Db 1 AASNLES 7

## RESULT 2

US-08-483-632-18  
; Sequence 18, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-632-18

Query Match 100.0%; Score 31; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
| | | | |  
Db 1 AASNLES 7

## RESULT 3

US-08-984-277-6

; Sequence 6, Application US/08984277  
; Patent No. 6057421  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Sybille  
; APPLICANT: Kohler, Heinz  
; TITLE OF INVENTION: VARIABLE HEAVY AND LIGHT CHAIN REGIONS OF MURINE  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1F7  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/984,277  
; FILING DATE: 3-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bucca, Daniel  
; REGISTRATION NUMBER: 42,368  
; REFERENCE/DOCKET NUMBER: 50200-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-756-8600  
; TELEFAX: 202-756-8699  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-984-277-6

Query Match 100.0%; Score 31; DB 3; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
| | | | |  
Db 12 AASNLES 18

## RESULT 4

US-08-466-151-6  
; Sequence 6, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

us-09-701-001b-5.ra1

Fri Feb 14 15:00:56 2003

SOFTWARE: WinPattn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,151  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/466163  
 FILING DATE: 06-Jun-1995  
 APPLICATION NUMBER: 08/405617  
 FILING DATE: 15-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/185899  
 FILING DATE: 26-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/879495  
 FILING DATE: 07-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: P0718P2C1D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 106 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-466-151-6

Query Match 100.0%; Score 31; DB 3; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 4.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
 Db 54 AASNLES 60

RESULT 5  
 US-08-466-163B-6  
 ; Sequence 6, Application US/08466163B  
 ; Patent No. 6329509  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; TITLE OF INVENTION: Immunoglobulin Variants  
 ; FILE REFERENCE: P0718P2C1D1  
 ; CURRENT APPLICATION NUMBER: US/08/466,163B  
 ; CURRENT FILING DATE: 1995-06-06  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 6  
 ; LENGTH: 106  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-08-466-163B-6

Query Match 100.0%; Score 31; DB 4; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 4.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7

Db 54 AASNLES 60

RESULT 6  
 US-08-491-845-8  
 ; Sequence 8, Application US/08491845  
 ; Patent No. 5773247  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAEDA, Hiroaki  
 ; APPLICANT: KIMACHI, Kazuhiko  
 ; APPLICANT: EDA, Yasuyuki  
 ; APPLICANT: SHIOSAKI, Kouichi  
 ; APPLICANT: OSATOMI, Kiyoshi  
 ; APPLICANT: TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND  
 ; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Browdy and Neimark  
 ; STREET: 419 Seventh Street N.W. Ste. 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/491,845  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/JP93/00039  
 ; FILING DATE: 14-JAN-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Browdy, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: MAEDA=5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 628-5197  
 ; TELEFAX: (202) 737-3528  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 111 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-491-845-8

Query Match 100.0%; Score 31; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
 Db 54 AASNLES 60

RESULT 7  
 US-08-491-845-16  
 ; Sequence 16, Application US/08491845  
 ; Patent No. 5773247  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MAEDA, Hiroaki  
 ; APPLICANT: KIMACHI, Kazuhiko  
 ; APPLICANT: EDA, Yasuyuki  
 ; APPLICANT: SHIOSAKI, Kouichi  
 ; APPLICANT: OSATOMI, Kiyoshi  
 ; APPLICANT: TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: RECOMBINANT ANTI-HIV ANTIBODY AND

```

; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,845
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00039
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: MAEDA-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-845-16

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Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AASNLES 7
Db 54 AASNLES 60

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## RESULT 8

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US-08-483-636-73
; Sequence 73, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:

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; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITL OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-483-636-73

```

```

Query Match 100.0%; Score 31; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AASNLES 7
Db 54 AASNLES 60

```

## RESULT 9

```

US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:

```

```

; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITL OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.

```

REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-483-632-73

Query Match 100.0%; Score 31; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AASNLES 7  
|||||||  
54 AASNLES 60

RESULT 10  
US-08-513-968-51  
; Sequence 51, Application US/08513968  
; Patent No. 6114143  
; GENERAL INFORMATION:  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: MAKIZUMI, Keiichi  
; APPLICANT: SHIOSAKI, Kouichi  
; APPLICANT: OSATOMI, Kiyoshi  
; APPLICANT: KINACHL, Kazuhiko  
; APPLICANT: HIGUCHI, Hirofumi  
; APPLICANT: TORIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NETMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,968  
FILING DATE: 11-SEP-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 78913/1993  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: EDA-1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633

INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 115 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-513-968-51

Query Match 100.0%; Score 31; DB 3; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 58 AASNLES 64  
|||||||

RESULT 11  
US-08-483-636-14  
; Sequence 14, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,636  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-636-14

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 73 AASNLES 79  
|||||||

RESULT 12  
US-08-483-636-58  
; Sequence 58, Application US/08483636

; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-636-58

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
Db 73 AASNLES 79

RESULT 13  
US-08-483-632-14  
; Sequence 14, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:

; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-632-14

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AASNLES 7  
Db 73 AASNLES 79

RESULT 14  
US-08-483-632-58  
; Sequence 58, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:



CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-632-58

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 73 AASNLES 79

RESULT 15  
US-08-589-939-3  
Sequence 3, Application us/08589939  
Patent No. 6015662  
GENERAL INFORMATION:  
APPLICANT: Hackett, Jr., John R.  
APPLICANT: Hoff, Jane A.  
APPLICANT: Ostrow, David H.  
APPLICANT: Golden, Alan M.  
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND  
TITLE OF INVENTION: CONTROLS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: US  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: .US/08/589,939  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5865.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-935-1729  
TELEFAX: 847-938-2623  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid

Query Match 100.0%; Score 31; DB 3; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 74 AASNLES 80

Search completed: February 14, 2003, 11:20:50  
Job time : 7.32258 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model  
Run on: February 14, 2003, 11:15:53 ; Search time 4.06452 Seconds  
(without alignments)  
44.001 Million cell updates/sec

Title: US-09-701-001b-5  
Perfect score: 31  
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pap:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pap:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description       |
|------------|-------|---------------|--------|-------|-------------------|
| 1          | 31    | 100.0         | 7      | 9     | US-09-879-461-18  |
| 2          | 31    | 100.0         | 106    | 10    | US-09-802-077-6   |
| 3          | 31    | 100.0         | 106    | 10    | US-09-802-096-6   |
| 4          | 31    | 100.0         | 131    | 9     | US-09-879-461-14  |
| 5          | 31    | 100.0         | 131    | 9     | US-09-879-461-58  |
| 6          | 31    | 100.0         | 132    | 9     | US-09-879-461-2   |
| 7          | 31    | 100.0         | 218    | 10    | US-09-917-410-2   |
| 8          | 31    | 100.0         | 238    | 9     | US-09-903-327A-4  |
| 9          | 28    | 90.3          | 111    | 9     | US-09-144-886-93  |
| 10         | 28    | 90.3          | 112    | 9     | US-09-144-886-95  |
| 11         | 27    | 87.1          | 20     | 10    | US-09-839-447A-19 |
| 12         | 27    | 87.1          | 20     | 10    | US-09-839-447A-20 |
| 13         | 27    | 87.1          | 112    | 9     | US-09-144-886-80  |
| 14         | 27    | 87.1          | 112    | 9     | US-09-144-886-81  |
| 15         | 27    | 87.1          | 112    | 9     | US-09-144-886-84  |
| 16         | 27    | 87.1          | 112    | 9     | US-09-144-886-85  |
| 17         | 27    | 87.1          | 112    | 9     | US-09-144-886-86  |
| 18         | 27    | 87.1          | 112    | 9     | US-09-144-886-94  |
| 19         | 27    | 87.1          | 112    | 10    | US-09-810-502-36  |

|    |      |      |    |                     |                   |
|----|------|------|----|---------------------|-------------------|
| 20 | 87.1 | 112  | 10 | US-09-810-502-37    | Sequence 37, Appl |
| 21 | 87.1 | 129  | 10 | US-09-839-447A-2    | Sequence 2, Appli |
| 22 | 87.1 | 619  | 10 | US-09-800-065-2     | Sequence 2, Appli |
| 23 | 83.9 | 108  | 10 | US-09-056-160B-12   | Sequence 12, Appl |
| 24 | 83.9 | 109  | 10 | US-09-811-123-6     | Sequence 6, Appli |
| 25 | 83.9 | 111  | 10 | US-09-920-171-7     | Sequence 7, Appli |
| 26 | 83.9 | 263  | 9  | US-09-956-086-3     | Sequence 3, Appli |
| 27 | 83.9 | 263  | 9  | US-09-956-087-3     | Sequence 3, Appli |
| 28 | 83.9 | 283  | 9  | US-09-985-442-6     | Sequence 6, Appli |
| 29 | 83.9 | 283  | 10 | US-09-983-580-6     | Sequence 6, Appli |
| 30 | 83.9 | 721  | 10 | US-09-727-801-14    | Sequence 14, Appl |
| 31 | 80.6 | 105  | 10 | US-09-864-761-38594 | Sequence 38594, A |
| 32 | 80.6 | 518  | 10 | US-09-841-132-333   | Sequence 333, App |
| 33 | 80.6 | 554  | 10 | US-09-864-761-37625 | Sequence 37625, A |
| 34 | 80.6 | 875  | 10 | US-09-848-035-16    | Sequence 16, Appl |
| 35 | 80.6 | 875  | 10 | US-09-986-224-16    | Sequence 16, Appl |
| 36 | 80.6 | 894  | 9  | US-09-754-853A-1099 | Sequence 1099, Ap |
| 37 | 80.6 | 894  | 9  | US-09-754-853A-1116 | Sequence 1116, Ap |
| 38 | 80.6 | 894  | 9  | US-09-754-853A-1117 | Sequence 1117, Ap |
| 39 | 80.6 | 894  | 9  | US-09-754-853A-1118 | Sequence 1118, Ap |
| 40 | 80.6 | 894  | 9  | US-09-754-853A-1119 | Sequence 1119, Ap |
| 41 | 80.6 | 1751 | 10 | US-09-841-132-445   | Sequence 445, App |
| 42 | 80.6 | 1751 | 10 | US-09-841-132-594   | Sequence 594, App |
| 43 | 80.6 | 1752 | 10 | US-09-841-132-180   | Sequence 180, App |
| 44 | 80.6 | 3256 | 10 | US-09-919-172-98    | Sequence 98, Appl |
| 45 | 77.4 | 7    | 9  | US-09-968-561A-185  | Sequence 185, App |

## ALIGNMENTS

RESULT 1  
US-09-879-461-18  
; Sequence 18, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; Swedeland Rd.  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,461  
; FILING DATE: 12-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,929  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/136,783  
; FILING DATE: 14-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-879-461-18

Query Match 100.0%; Score 31; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
Db 1 AASNLES 7

## RESULT 2

US-09-802-077-6  
; Sequence 6, Application US/09802077  
; Patent No. US20010033842A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C20S

; CURRENT APPLICATION NUMBER: US/09/802,077  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14

; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 6  
; LENGTH: 106  
; TYPE: PRT

; ORGANISM: Mus musculus  
US-09-802-077-6

Query Match 100.0%; Score 31; DB 10; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
54 AASNLES 60

## RESULT 3

US-09-802-096-6  
; Sequence 6, Application US/09802096  
; Patent No. US20010033839A1  
; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C30S  
; CURRENT APPLICATION NUMBER: US/09/802,096  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768

; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 6  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-802-096-6

Query Match 100.0%; Score 31; DB 10; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
Db 54 AASNLES 60

## RESULT 4

US-09-879-461-14  
; Sequence 14, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:

; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.

; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; Swedeland Rd.

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-2799

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/879,461

; FILING DATE: 12-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/612,929

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/136,783

; FILING DATE: 14-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34,028

; REFERENCE/DOCKET NUMBER: P50186-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 270-5024

; TELEFAX: (215) 270-5090

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 131 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-879-461-14

Query Match

100.0%; Score 31; DB 9; Length 131;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
| | | | |  
Db 73 AASNLES 79

RESULT 5  
US-09-879-461-58  
; Sequence 58, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; Swedeland Rd.  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,461  
; FILING DATE: 12-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,929  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/136,783  
; FILING DATE: 14-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-09-879-461-58  
Query Match 100.0%; Score 31; DB 9; Length 131;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AASNLES 7  
Db 73 AASNLES 79  
RESULT 6  
US-09-879-461-2  
; Sequence 2, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation

STREET: Corporate Intellectual Property, UW2220 - 709  
Swedeland Rd.  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,461  
FILING DATE: 12-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/612,929  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/136,783  
FILING DATE: 14-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-879-461-2  
Query Match 100.0%; Score 31; DB 9; Length 132;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AASNLES 7  
Db 74 AASNLES 80  
RESULT 7  
US-09-917-410-2  
; Sequence 2, Application US/09917410  
; Patent No. US20020098183A1  
; GENERAL INFORMATION:  
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;  
; CO, Man S.  
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF  
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR  
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER  
; EXTRACORPOREAL BLOOD CIRCULATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII, WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/917,410  
; FILING DATE: 26-Jul-2001  
; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/578,953  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: EP 95 114 969.9  
;; FILING DATE: 19-Sep-95  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hanson, No. US20020098183Alman D.  
;; REGISTRATION NUMBER: 30,946  
;; REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 688-3200  
;; TELEFAX: (212) 838-3884  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 218  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-917-410-2

Query Match 100.0%; Score 31; DB 10; Length 218;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 8  
US-09-903-327A-4  
; Sequence 4, Application US/09903327A  
; Patent No. US20020164333A1  
; GENERAL INFORMATION:  
; APPLICANT: Nemerow, Glen R.  
; APPLICANT: Li, Erquang  
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET  
; TITLE OF INVENTION: GENE  
; FILE REFERENCE: 22908-1228  
; CURRENT APPLICATION NUMBER: US/09/903,327A  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 09/613,017  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody  
US-09-903-327A-4

Query Match 100.0%; Score 31; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 74 AASNLES 80

RESULT 9  
US-09-144-886-93  
; Sequence 93, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D

; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone  
; OTHER INFORMATION: ICG region VL epitope 3  
US-09-144-886-93

Query Match 90.3%; Score 28; DB 9; Length 111;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 10  
US-09-144-886-95  
; Sequence 95, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 95  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone  
; OTHER INFORMATION: IG5 region VL epitope 3  
US-09-144-886-95

Query Match 90.3%; Score 28; DB 9; Length 112;  
Best Local Similarity 85.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

RESULT 11  
US-09-839-447A-19  
; Sequence 19, Application US/09839447A  
; Patent No. US20020058247A1  
; GENERAL INFORMATION:  
; APPLICANT: Sallberg, Matti  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE  
; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS  
; FILE REFERENCE: TRIPEP.020CPI  
; CURRENT APPLICATION NUMBER: US/09/839,447A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/556605  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-19

Query Match      87.1%; Score 27; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
Db  15 ASNLES 20

RESULT 12
US-09-839-447A-20
; Sequence 20, Application US/09839447A
; Patent No. US20020058247A1
; GENERAL INFORMATION:
; APPLICANT: Saliberg, Matti
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPEP.020CP1
; CURRENT APPLICATION NUMBER: US/09/839,447A
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/556605
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-20

Query Match      87.1%; Score 27; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
    5 ASNLES 10

RESULT 13
US-09-144-886-80
; Sequence 80, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-80

Query Match      87.1%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
    55 ASNLES 60

RESULT 14
US-09-144-886-81
; Sequence 81, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-81

Query Match      87.1%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
    55 ASNLES 60

RESULT 15
US-09-144-886-84
; Sequence 84, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-84

Query Match      87.1%; Score 27; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 ASNLES 7
    55 ASNLES 60

Search completed: February 14, 2003, 11:21:31
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Fri Feb 14 15:00:57 2003

us-09-701-001b-5.rapb

Page 6

Job time : 4.06452 secs



GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 7 seconds  
(without alignments)

96.134 Million cell updates/sec

Title: US-09-701-001b-5

Perfect score: 31

Sequence: 1 AASNLES 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*

1: pirl:\*

2: pirl:\*

3: pirl:\*

4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description          |
|------------|-------|-------------|--------|----------|----------------------|
| 1          | 31    | 100.0       | 65     | 2 C38601 | Ig kappa chain V r   |
| 2          | 31    | 100.0       | 65     | 2 B38601 | Ig kappa chain V r   |
| 3          | 31    | 100.0       | 93     | 2 A38601 | Ig kappa chain V r   |
| 4          | 31    | 100.0       | 110    | 1 KVM510 | Ig kappa chain V r   |
| 5          | 31    | 100.0       | 111    | 1 KVM5C1 | Ig kappa chain V r   |
| 6          | 31    | 100.0       | 111    | 1 KVM543 | Ig kappa chain V r   |
| 7          | 31    | 100.0       | 111    | 1 KVM583 | Ig kappa chain V r   |
| 8          | 31    | 100.0       | 111    | 1 KVM569 | Ig kappa chain V r   |
| 9          | 31    | 100.0       | 112    | 2 S19971 | Ig kappa chain V r   |
| 10         | 31    | 100.0       | 112    | 2 S19976 | Ig kappa chain V r   |
| 11         | 31    | 100.0       | 131    | 2 PH1226 | Ig kappa chain pre   |
| 12         | 31    | 100.0       | 463    | 2 B64160 | hypothetical prote   |
| 13         | 31    | 100.0       | 942    | 2 T39624 | 6-phosphofructokin   |
| 14         | 31    | 100.0       | 1208   | 2 T00362 | hypothetical prote   |
| 15         | 28    | 90.3        | 69     | 2 AH3440 | cold shock protein   |
| 16         | 28    | 90.3        | 108    | 1 K1HUGL | Ig kappa chain V-I   |
| 17         | 28    | 90.3        | 112    | 2 S19972 | Ig kappa chain V r   |
| 18         | 28    | 90.3        | 120    | 2 S06731 | Ig kappa chain pre   |
| 19         | 28    | 90.3        | 122    | 2 S40370 | Ig kappa chain - h   |
| 20         | 28    | 90.3        | 209    | 2 C87521 | hypothetical prote   |
| 21         | 28    | 90.3        | 228    | 2 A98166 | hypothetical prote   |
| 22         | 28    | 90.3        | 228    | 2 AF3121 | hypothetical prote   |
| 23         | 28    | 90.3        | 313    | 1 QMXRWT | capsomere protein    |
| 24         | 28    | 90.3        | 313    | 1 QMXRWN | nonstructural prot   |
| 25         | 28    | 90.3        | 579    | 2 AB2177 | hypothetical prote   |
| 26         | 28    | 90.3        | 632    | 2 D71941 | ATP-dependent zinc   |
| 27         | 28    | 90.3        | 784    | 1 A55236 | kinesin-related pr   |
| 28         | 27    | 87.1        | 81     | 2 S42193 | Ig kappa chain V r   |
| 29         | 27    | 87.1        | 91     | 2 S25462 | - Ig kappa chain V r |

#### ALIGNMENTS

##### RESULT 1

C38601

Ig kappa chain V region (2B5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999

C;Accession: C38601

R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same anti

A;Reference number: A38601; MUID:91115823; PMID:1703527

A;Accession: C38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-65 <GOS>

A;Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;

Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0;

QY 1 AASNLES 7

Db 7 AASNLES 13

##### RESULT 2

B38601

Ig kappa chain V region (7D4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999

C;Accession: B38601

R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A;Title: Common structural features among monoclonal antibodies binding the same anti

A;Reference number: A38601; MUID:91115823; PMID:1703527

A;Accession: B38601

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-65 <GOS>

A;Cross-references: GB:M57979; NID:g196404; PIDN:AAA63360.1; PID:g196405

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 65;

Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0;

QY 1 AASNLES 7

Db 7 AASNLES 13

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60  
|||||

RESULT 6  
KVMS43  
Ig kappa chain V region (PC7043) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
C:Accession: A01937; S42187; S42194; S42190; S42189; S42188; S42191; S42192  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152; PMID:103003  
A:Accession: A01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993  
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s  
A:Reference number: S42176; MUID:94009207; PMID:7691608  
A:Accession: S42187  
A:Molecule type: DNA  
A:Residues: 10-99 <MOJ>  
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833  
A:Note: V-kappa-2IE; anti-collagen  
A:Accession: S42194  
A:Molecule type: DNA  
A:Residues: 12-99 <MOJ>  
A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845  
A:Note: V-kappa-2IE; anti-collagen  
A:Accession: S42190  
A:Molecule type: DNA  
A:Residues: 13-99 <MOJ>  
A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839  
A:Note: V-kappa-2IE; anti-collagen  
A:Accession: S42189  
A:Molecule type: DNA  
A:Residues: 15-99 <MOA>  
A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837  
A:Note: V-kappa-2IE; anti-collagen  
A:Accession: S42188  
A:Molecule type: DNA  
A:Residues: 12-99 <MOJ>  
A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835  
A:Note: V-kappa-2IE; anti-collagen  
A:Accession: S42191  
A:Molecule type: DNA  
A:Residues: 10-99 <MOJ>  
A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841  
A:Note: V-kappa-2IE; anti-collagen  
A:Accession: S42192  
A:Molecule type: DNA  
A:Residues: 10-99 <MOJ>  
A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843  
A:Note: V-kappa-2IE; anti-collagen  
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

RESULT 3  
A38601  
Ig kappa chain V region (IG3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999  
C:Accession: A38601  
R:Goshorn, S.C.; Retzel, E.; Jemmerson, R.  
J. Biol. Chem. 266, 2134-2142, 1991  
A:Title: Common structural features among monoclonal antibodies binding the same antigen  
A:Reference number: A38601; MUID:91115823; PMID:1703527  
A:Accession: A38601  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-93 <GOS>  
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 35 AASNLES 41  
|||||

RESULT 4  
KVMS10  
Ig kappa chain V region (PC7210) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: D01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152; PMID:103003  
A:Accession: D01937  
A:Molecule type: protein  
A:Residues: 1-110 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60  
|||||

RESULT 5  
KVMS1  
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000  
C:Accession: A01936  
R:McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related mo  
A:Reference number: A93822; MUID:79012520; PMID:99744  
A:Accession: A01936  
A:Molecule type: protein  
A:Residues: 1-111 <MCK>  
A:Comment: This chain was isolated from a myeloma protein.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

## RESULT 7

KWS83

Ig kappa chain V region (PC7183) - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000

C:Accession: B01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Gene 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: B01937

A:Molecule type: protein

A:Residues: 1-111 &lt;WEI&gt;

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology &lt;IMM&gt;

F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

## RESULT 8

KWS69

Ig kappa chain V region (PC7769) - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000

C:Accession: B01937; A01937

R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.

Gene 276, 785-790, 1978

A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.

A:Reference number: A93204; MUID:79073152; PMID:103003

A:Accession: B01937

A:Molecule type: protein

A:Residues: 1-111 &lt;WEI&gt;

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology &lt;IMM&gt;

F:23-92/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

## RESULT 9

S19971

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S19971; S19973  
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: S19963  
A:Accession: S19971  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289  
A:Experimental source: clone M-T310  
A:Accession: S19973  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEW>  
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293  
A:Experimental source: M-T404  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

## RESULT 10

S19976

Ig kappa chain V region (M-T413) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S19976

R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

A:Accession: S19976

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 &lt;WEI&gt;

A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-94/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 31; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
Db 54 AASNLES 60

## RESULT 11

PH1226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000

C:Accession: PH1226

R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L

Gene 121, 271-278, 1992

A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and

A:Reference number: PH1224; MUID:93077041; PMID:1446824

A:Accession: PH1226

A:Molecule type: mRNA

A:Residues: 1-131 &lt;WEI&gt;

A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766

A:Note: this mouse sequence was hybridized and fused with a human constant region gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-131/Product: Ig light chain V region #status predicted <MAT>  
F;36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 31; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
|||||  
Db 74 AASNLES 80

## RESULT 12

B64160  
hypothetical protein HI0852 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 26-Aug-1999  
C:Accession: B64160  
R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
M.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Genbank 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: B64160  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-463 <TIGR>  
A:Cross-references: GB:U32766; GB:L42023; NID:gl573854; PIDN:AAC22509.1; PID:gl573866; T  
A:Note: best homolog was a hypothetical protein from Escherichia coli  
C:Superfamily: multidrug-efflux transporter  
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 100.0%; Score 31; DB 2; Length 463;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
|||||  
Db 94 AASNLES 100

## RESULT 13

T39624  
6-phosphofructokinase beta subunit - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
C:Accession: T39624  
R:God, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
Submitted to the EMBL Data Library, March 1998  
A:Reference number: Z21843  
A:Accession: T39624  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-942 <WOO>  
A:Cross-references: EMBL:AL022104; PIDN:CAA17900.1; GSPDB:GN00067; SPDB:SPBC16H5.02  
A:Experimental source: strain 972h; cosmid c16H5  
C:Genetics:  
A:Gene: SPDB:SPBC16H5.02  
A:Map position: 2  
C:Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology

Query Match 100.0%; Score 31; DB 2; Length 942;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
|||||  
Db 165 AASNLES 171

## RESULT 14

T00362  
hypothetical protein KIAA0675 - human  
C:Species: Homo sapiens (man)  
C>Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 02-Sep-2000  
C:Accession: T00362  
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura,  
DNA Res. 5, 169-176, 1998  
A:Title: Prediction of the coding sequences of unidentified human genes. X. The compl  
A:Reference number: Z14142; MUID:98403880; PMID:9734811  
A:Accession: T00362  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1208 <ISH>  
A:Cross-references: EMBL:AB014575; NID:g3327163; PIDN:BAA31650.1; PID:g3327164  
A:Experimental source: brain; clone HK02566  
C:Genetics:  
A:Note: KIAA0675  
C:Superfamily: RING finger homology  
F:1144-1193/Domain: RING finger homology <RRN>

Query Match 100.0%; Score 31; DB 2; Length 1208;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
|||||  
Db 896 AASNLES 902

## RESULT 15

AH3440  
cold shock protein csps [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 17-May-2002  
C:Accession: AH3440  
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov  
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AH3440  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-69 <KUR>  
A:Cross-references: GB:AE008917; PIDN:AAL52691.1; PID:gl7983518; GSPDB:GN00190  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEI1510  
A:Map position: 1  
C:Superfamily: major cold shock protein; cold shock domain homology

Query Match 90.3%; Score 28; DB 2; Length 69;  
Best Local Similarity 85.7%; Pred. No. 5.5;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
|||||  
Db 62 AASNLES 68

Search completed: February 14, 2003, 11:19:47  
Job time : 7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model  
Run on: February 14, 2003, 11:05:27 ; Search time 3.6129 Seconds  
(without alignments)  
80.360 Million cell updates/sec

Title: US-09-701-001B-5  
Perfect score: 31  
Sequence: 1 AASNLES 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result NO. | Score | Query Match % | Length | DB ID        | Description         |
|------------|-------|---------------|--------|--------------|---------------------|
| 1          | 31    | 100.0         | 110    | 1 KV3P_MOUSE | P01668 mus musculus |
| 2          | 31    | 100.0         | 111    | 1 KV3L_MOUSE | P01664 mus musculus |
| 3          | 31    | 100.0         | 111    | 1 KV3M_MOUSE | P01665 mus musculus |
| 4          | 31    | 100.0         | 111    | 1 KV3N_MOUSE | P01666 mus musculus |
| 5          | 31    | 100.0         | 111    | 1 KV3Q_MOUSE | P01669 mus musculus |
| 6          | 31    | 100.0         | 463    | 1 YIEQ_HAEIN | P44903 haemophilus  |
| 7          | 28    | 90.3          | 108    | 1 KVIQ_HUMAN | P01599 homo sapien  |
| 8          | 28    | 90.3          | 313    | 1 VP9_WTV    | P12326 wound tumor  |
| 9          | 28    | 90.3          | 313    | 1 FTSH_HELPJ | Q92m66 helicobacte  |
| 10         | 28    | 90.3          | 632    | 1 KL68_DROME | P01594 homo sapien  |
| 11         | 28    | 87.1          | 108    | 1 KVI8_HUMAN | P01564 mus musculus |
| 12         | 27    | 87.1          | 108    | 1 KV3H_MOUSE | P01660 mus musculus |
| 13         | 27    | 87.1          | 111    | 1 KV3J_MOUSE | P01662 mus musculus |
| 14         | 27    | 87.1          | 111    | 1 KV3K_MOUSE | P01663 mus musculus |
| 15         | 27    | 87.1          | 111    | 1 KV3L_MOUSE | P01664 mus musculus |
| 16         | 27    | 87.1          | 111    | 1 KV3M_MOUSE | P01665 mus musculus |
| 17         | 27    | 87.1          | 111    | 1 KV3N_MOUSE | P01666 mus musculus |
| 18         | 27    | 87.1          | 111    | 1 KV3Q_MOUSE | P01669 mus musculus |
| 19         | 27    | 87.1          | 111    | 1 KV3R_MOUSE | P01670 mus musculus |
| 20         | 27    | 87.1          | 111    | 1 KV3S_MOUSE | P01671 mus musculus |
| 21         | 27    | 87.1          | 131    | 1 KV3T_MOUSE | P01672 mus musculus |
| 22         | 27    | 87.1          | 177    | 1 PSS_BACSU  | P39823 bacillus su  |
| 23         | 27    | 87.1          | 230    | 1 CUTL_FUSSO | P00590 fusarium so  |
| 24         | 27    | 87.1          | 230    | 1 CUTL_FUSSC | Q99174 fusarium so  |
| 25         | 27    | 87.1          | 260    | 1 UPPS_BACSU | Q31751 bacillus su  |
| 26         | 27    | 87.1          | 396    | 1 PGK_LISIN  | Q92810 listeria in  |
| 27         | 27    | 87.1          | 396    | 1 PGK_LISMO  | Q8y4i2 listeria mo  |
| 28         | 27    | 87.1          | 486    | 1 YN8U_YEAST | P53742 saccharomyc  |
| 29         | 27    | 87.1          | 661    | 1 UVRB_RICCN | Q92j03 rickettsia   |
| 30         | 27    | 87.1          | 662    | 1 UVRB_RICPR | Q92dw2 rickettsia   |
| 31         | 27    | 87.1          | 689    | 1 UVRB_HALN1 | Q9hmt9 halobacteri  |
| 32         | 26    | 83.9          | 112    | 1 KV3G_MOUSE | P01659 mus musculus |
| 33         | 26    | 83.9          | 132    | 1 KV3F_MOUSE | P01658 mus musculus |

|    |    |      |      |              |                    |
|----|----|------|------|--------------|--------------------|
| 34 | 26 | 83.9 | 292  | 1 SNAP_DROME | Q23983 drosophila  |
| 35 | 26 | 83.9 | 456  | 1 KICH_HUMAN | P35790 homo sapien |
| 36 | 26 | 83.9 | 1407 | 1 CYAA_DICDI | Q03100 dictyosteli |
| 37 | 26 | 83.9 | 2017 | 1 MYSN_DROME | Q99323 drosophila  |
| 38 | 25 | 80.6 | 259  | 1 FLA2_NATMA | Q93718 natrialba m |
| 39 | 25 | 80.6 | 295  | 1 PYRB_CAMJE | O9pj16 campylobact |
| 40 | 25 | 80.6 | 313  | 1 CDX2_HUMAN | O99626 homo sapien |
| 41 | 25 | 80.6 | 313  | 1 CDX2_MESAU | Q04649 mesocricetu |
| 42 | 25 | 80.6 | 334  | 1 CHM1_RAT   | O70367 rattus norv |
| 43 | 25 | 80.6 | 362  | 1 ALEU_HORVU | P05167 hordeum vul |
| 44 | 25 | 80.6 | 397  | 1 AAT_STRVG  | Q60013 streptomyce |
| 45 | 25 | 80.6 | 426  | 1 HISX_METTH | O26327 methanobact |

## ALIGNMENTS

### RESULT 1

| ID | KV3P_MOUSE   | STANDARD; | PRT; | 110 AA. |
|----|--|-----------|------|---------|
| AC | P01668;  |           |      |         |
| DT | 21-JUL-1986 (Rel. 01, Created)                                     |           |      |         |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update)                        |           |      |         |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update)                      |           |      |         |
| DE | Ig kappa chain V-III region PC 7210.                               |           |      |         |
| OS | Mus musculus (Mouse).  |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |           |      |         |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |           |      |         |
| OX | NCBI_TaxID=10090;  |           |      |         |
| RN | [1]  |           |      |         |
| RP | SEQUENCE.  |           |      |         |
| RX | MEDLINE=79073152; PubMed=103003;                                   |           |      |         |
| RA | Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;         |           |      |         |
| RT | "Rearrangement of genetic information may produce immunoglobulin   |           |      |         |
| RT | diversity."  |           |      |         |
| RL | Nature 276:785-790(1978).  |           |      |         |
| DR | PIR; D01937; KVM510.   |           |      |         |
| DR | HSSP; P01679; 2FBJ.  |           |      |         |
| DR | InterPro; IPR003006; Ig_MHC.                                       |           |      |         |
| DR | PIfam; PF00047; Ig; 1.   |           |      |         |
| DR | SMART; SM00406; Ig; 1.   |           |      |         |
| KW | Immunoglobulin V region.   |           |      |         |
| FT | DOMAIN 1 23  |           |      |         |
| FT | DOMAIN 24 38   |           |      |         |
| FT | DOMAIN 29 53   |           |      |         |
| FT | DOMAIN 54 60   |           |      |         |
| FT | DOMAIN 61 92   |           |      |         |
| FT | DOMAIN 93 100  |           |      |         |
| FT | DOMAIN 101 110   |           |      |         |
| FT | DISULFID 23 92   |           |      |         |
| FT | NON_TER 110 110  |           |      |         |
| SQ | SEQUENCE 110 AA; 69FIA5CE886B1249 CRC64;                           |           |      |         |

Query Match 100.0%; Score 31; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.86;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

### QY 1 AASNLES 7

Db 54 AASNLES 60

### RESULT 2

| ID | KV3L_MOUSE  | STANDARD; | PRT; | 111 AA. |
|----|---|-----------|------|---------|
| AC | P01664;   |           |      |         |
| DT | 21-JUL-1986 (Rel. 01, Created)                                    |           |      |         |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update)                       |           |      |         |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update)                     |           |      |         |
| DE | Ig kappa chain V-III region CBPC 101.                             |           |      |         |
| OS | Mus musculus (Mouse).   |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |           |      |         |

|                       |  |                 |       |                                 |
|-----------------------|--|-----------------|-------|---------------------------------|
| Query Match           | 100.0%;  | Score 31;       | DB 1; | Length 111;                     |
| Best Local Similarity | 100.0%;  | Pred. No. 0.87; |       |                                 |
| Matches               | 7;   | Conservative    | 0;    | Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 1  | AASNLES 7       |       |                                 |
| Db                    | 54   | AASNLES 60      |       |                                 |
|                       |  |                 |       |                                 |
| RESULT 4              |  |                 |       |                                 |
| KV3N_MOUSE            |  | STANDARD;       | PRT;  | 111 AA.                         |
| ID                    | KV3N_MOUSE   |                 |       |                                 |
| AC                    | P01666;  |                 |       |                                 |
| DT                    | 21-JUL-1986 (Rel. 01, Created)                                     |                 |       |                                 |
| DT                    | 21-JUL-1986 (Rel. 01, Last sequence update)                        |                 |       |                                 |
| DT                    | 15-JUL-1999 (Rel. 38, Last annotation update)                      |                 |       |                                 |
| DE                    | Ig kappa chain V-III region PC 7183.                               |                 |       |                                 |
| OS                    | Mus musculus (Mouse).  |                 |       |                                 |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                 |       |                                 |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |                 |       |                                 |
| OX                    | NCBI_TaxID=10090;  |                 |       |                                 |
| RN                    | [1]  |                 |       |                                 |
| RP                    | SEQUENCE.  |                 |       |                                 |
| RX                    | MEDLINE=79073152; PubMed=103003;                                   |                 |       |                                 |
| RA                    | Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;         |                 |       |                                 |
| RT                    | "Rearrangement of genetic information may produce immunoglobulin   |                 |       |                                 |
| RT                    | diversity."  |                 |       |                                 |
| RL                    | Nature 276;785-790(1978).  |                 |       |                                 |
| DR                    | HSP; P01679; 2FBJ.   |                 |       |                                 |
| DR                    | InterPro; IPR003006; Ig_MHC.                                       |                 |       |                                 |
| DR                    | Pfam; PF00047; Ig_1.   |                 |       |                                 |
| DR                    | SMART; SM00406; IGv; 1.  |                 |       |                                 |
| KW                    | Immunoglobulin V region.   |                 |       |                                 |
| FT                    | DOMAIN 1 23  |                 |       |                                 |
| FT                    | DOMAIN 24 38   |                 |       |                                 |
| FT                    | DOMAIN 39 53   |                 |       |                                 |
| FT                    | DOMAIN 54 60   |                 |       |                                 |
| FT                    | DOMAIN 61 92   |                 |       |                                 |
| FT                    | DOMAIN 93 101  |                 |       |                                 |
| FT                    | DOMAIN 102 111   |                 |       |                                 |
| FT                    | DISULFID 23 92   |                 |       |                                 |
| FT                    | NON_TER 111 111  |                 |       |                                 |
| SQ                    | SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;                 |                 |       |                                 |
|                       |  |                 |       |                                 |
| Query Match           | 100.0%;  | Score 31;       | DB 1; | Length 111;                     |
| Best Local Similarity | 100.0%;  | Pred. No. 0.87; |       |                                 |
| Matches               | 7;   | Conservative    | 0;    | Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 1  | AASNLES 7       |       |                                 |
| Db                    | 54   | AASNLES 60      |       |                                 |
|                       |  |                 |       |                                 |
| RESULT 5              |  |                 |       |                                 |
| KV3Q_MOUSE            |  | STANDARD;       | PRT;  | 111 AA.                         |
| ID                    | KV3Q_MOUSE   |                 |       |                                 |
| AC                    | P01669;  |                 |       |                                 |
| DT                    | 21-JUL-1986 (Rel. 01, Created)                                     |                 |       |                                 |
| DT                    | 21-JUL-1986 (Rel. 01, Last sequence update)                        |                 |       |                                 |
| DT                    | 15-JUL-1999 (Rel. 38, Last annotation update)                      |                 |       |                                 |
| DE                    | Ig kappa chain V-III region PC 7769.                               |                 |       |                                 |
| OS                    | Mus musculus (Mouse).  |                 |       |                                 |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                 |       |                                 |
| OC                    | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |                 |       |                                 |
| OX                    | NCBI_TaxID=10090;  |                 |       |                                 |
| RN                    | [1]  |                 |       |                                 |
| RP                    | SEQUENCE.  |                 |       |                                 |
| RX                    | MEDLINE=79073152; PubMed=103003;                                   |                 |       |                                 |
| RA                    | Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;         |                 |       |                                 |
| RT                    | "Rearrangement of genetic information may produce immunoglobulin   |                 |       |                                 |

```

RT diversity";
RL Nature 276:785-790(1978).
DR PIR; E01937; KMS69.
DR HSP; F80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.87; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
DB 54 AASNLES 60

RESULT 6
ID YIEO_HAEIN STANDARD; PRT; 463 AA.
AC P44903.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical transport protein HI0852.
GN HI0852.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RY MEDLINE=95350630; PubMed=7542800;
RA Fieischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
(probable).
CC -!- SIMILARITY: STRONG, TO E.COLI YIEO.
CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
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CC EMBL; U32766; AAC22509.1; -.

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DR TIGR; HI0852; -.
DR InterPro; IPR004638; Efflux_EmrB.
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR TIGRFAMS; TIGR00711; efflux_EmrB; 1.
KW Hypothetical protein; transport; Transmembrane; Inner membrane;
Complete proteome.
FT TRANSMEM 10 30
FT TRANSMEM 49 69
FT TRANSMEM 82 102
FT TRANSMEM 107 127
FT TRANSMEM 139 159
FT TRANSMEM 165 185
FT TRANSMEM 197 217
FT TRANSMEM 225 245
FT TRANSMEM 267 287
FT TRANSMEM 298 318
FT TRANSMEM 328 348
FT TRANSMEM 354 374
FT TRANSMEM 393 413
FT TRANSMEM 429 449
FT TRANSMEM 463 AA; 50002 MW; D725EFDD50F9F23F CRC64;
SQ SEQUENCE 463 AA; 100.0%; Score 31; DB 1; Length 463;
Query Match 100.0%; Score 31; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 4.2; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 AASNLES 7
DB 94 AASNLES 100

RESULT 7
ID KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RY MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup 1."
RA Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR; A01867; K1HUGL.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 23 88
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

```

Query Match 90.3%; Score 28; DB 1; Length 108;  
 Best Local Similarity 85.7%; Pred. No. 4.8;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||||:  
 Db 50 AASNLSQ 56

RESULT 8  
 VP9\_WTV  
 ID VP9\_WTV STANDARD; PRT; 313 AA.  
 AC P12326;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Structural protein P9 (Capsomere protein P9) (Protein PNS11).  
 GN S11.  
 OS Wound tumor virus (WTV).  
 OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.  
 OX NCBI\_TaxID=10987;  
 [1]  
 SEQUENCE FROM N.A.  
 RA MEDLINE=89263810; PubMed=2726499;  
 RA Dall D.J., Anzola J.V., Xu Z., Nuss D.L.;  
 RT "Complete nucleotide sequence of wound tumor virus genomic segment  
 S11."  
 RL Nucleic Acids Res. 17:3599-3599(1989).  
 CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.  
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 CC  
 CC EMBL; X14219; CAA32439.1; -  
 DR PIR; S04139; QMXRWT.  
 SQ SEQUENCE 313 AA; 35606 MW; 6746F59840AD17F2 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;  
 Best Local Similarity 85.7%; Pred. No. 15;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||||:  
 Db 294 AASNLS 300

RESULT 9  
 VP9\_WTVNJ  
 ID VP9\_WTVNJ STANDARD; PRT; 313 AA.  
 AC P31611;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Structural protein P9 (Capsomere protein P9) (Protein PNS11).  
 OS Wound tumor virus (strain NJ) (WTV).  
 OC Viruses; dsRNA viruses; Reoviridae; Phytoreovirus.  
 OX NCBI\_TaxID=31595;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RA MEDLINE=92074261; PubMed=1962460;  
 RA Hillman B.I., Anzola J.V., Halpern B.T., Cavileer T.D., Nuss D.L.;  
 RT "First field isolation of wound tumor virus from a plant host:  
 RT minimal sequence divergence from the type strain isolated from an  
 RT insect vector."  
 RL Virology 185:896-900(1991).  
 CC -!- SIMILARITY: TO RICE DWARF VIRUS S9 AND RICE GALL DWARF VIRUS S10.  
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 CC  
 CC EMBL; M77020; AAA48500.1; -  
 DR PIR; C41705; QMXRWN  
 KW Nonstructural protein.  
 SQ SEQUENCE 313 AA; 35551 MW; D9B904785C601C34 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 313;  
 Best Local Similarity 85.7%; Pred. No. 15;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||||:  
 Db 294 AASNLS 300

RESULT 10  
 FTSH\_HELPJ  
 ID FTSH\_HELPJ STANDARD; PRT; 632 AA.  
 AC Q9ZM66;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cell division protein ftsh homolog (EC 3.4.24.-).  
 GN FTSH OR JHP0356.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxID=85963;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori.";  
 RL Nature 397:176-180(1999).  
 CC -!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE  
 CC (BY SIMILARITY).  
 CC -!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41.

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 CC  
 CC EMBL; AE001471; AAD05932.1; -  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003599; AAA\_ATPase\_centra.  
 DR InterPro; IPR003960; AAA\_sub.  
 DR InterPro; IPR000642; Peptidase\_M41.  
 DR Pfam; PF000004; AAA; 1  
 DR Pfam; PF01434; Peptidase\_M41; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR TIGRFAMs; TIGR01241; FtsH\_fam; 1.  
 DR PROSITE; PS00674; AAA; 1.  
 DR Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;  
 KW Zinc; Complete proteome.  
 CC DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).



FT TRANSMEM 10 31 POTENTIAL.  
 FT DOMAIN 32 116 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 117 137 POTENTIAL.  
 FT DOMAIN 138 632 CYTOPLASMIC (POTENTIAL).  
 FT NP\_BIND 210 217 ATP (POTENTIAL).  
 FT METAL 434 434 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT\_SITE 435 435 BY SIMILARITY.  
 FT METAL 438 438 ZINC (CATALYTIC) (BY SIMILARITY).  
 SQ SEQUENCE 632 AA; 69765 MW; 2FB67B43C51559FB CRC64;

Query Match 90.3%; Score 28; DB 1; Length 632;  
 Best Local Similarity 85.7%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||:||||  
 Db 616 AASNLES 622

RESULT 11  
 KL68\_DROME STANDARD; PRT; 784 AA.  
 AC F46867; Q9VTN8;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Kinesin-like protein KLP68D.  
 GN KLP68D OR KLP5 OR CG7293.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95050960; PubMed=7525600;  
 RA Pesavento P.A., Stewart R.J., Goldstein L.S.B.;  
 RT "Characterization of the KLP68D kinesin-like protein in Drosophila:  
 RP possible roles in axonal transport.";  
 RL J. Cell Biol. 127:1041-1048(1994).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,  
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 [3]  
 RN SEQUENCE OF 220-342 FROM N.A.  
 RP MEDLINE=92020874; PubMed=1924306;  
 RA Stewart R.J., Pesavento P.A., Woerpel D.N., Goldstein L.S.B.;  
 RT "Identification and partial characterization of six members of the  
 RT kinesin superfamily in Drosophila";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474(1991).  
 CC -!- FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR  
 CC ANTEROGRADE AXONAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN  
 CC FLY NEURONS DIFFERENT THAN THOSE MOVED BY KINESIN HEAVY CHAIN OR  
 CC OTHER PLUS-END DIRECTED MOTORS.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS  
 CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING  
 CC EMBRYOGENESIS.  
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN  
 CC II SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U15974; AAA69929.1; -;  
 DR EMBL; M74431; AAA28658.1; -;  
 DR EMBL; AE003543; AAF50008.1; -;  
 DR HSSP; P17119; 3KAR.  
 DR FlyBase; FBgn0004381; Klp68D.  
 DR InterPro; IPR001752; kinesin\_motor.  
 DR Pfam; PF00225; kinesin; 1.  
 DR PRINTS; PR00380; KINESINHEAVY.  
 DR SMART; SM00129; KISC; 1.  
 DR PROSITE; P500411; KINESIN\_MOTOR\_DOMAIN1; 1.  
 DR PROSITE; P50067; KINESIN\_MOTOR\_DOMAIN2; 1.  
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.  
 FT DOMAIN 16 275 KINESIN-MOTOR.  
 FT DOMAIN 351 385 COILED COIL (POTENTIAL).  
 FT DOMAIN 426 582 COILED COIL (POTENTIAL).  
 FT NP\_BIND 106 113 ATP (POTENTIAL).  
 FT CONFLICT 220 221 SS -> TC (IN REF. 3).  
 FT CONFLICT 338 342 GSRAK -> VRGOV (IN REF. 3).  
 FT CONFLICT 338 338 G -> A (IN REF. 2).  
 SQ SEQUENCE 784 AA; 88193 MW; 94BB9BADF072DFC0 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 784;  
 Best Local Similarity 85.7%; Pred. No. 42;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 |||||:  
 Db 751 AASNLES 757

RESULT 12  
 KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 ID KV1B\_HUMAN  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein Au).";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=77022433; PubMed=1234024;  
 RA Fehlhämmer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwager P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 RT Bence-Jones protein Au.";  
 RL Biophys. Struct. Mech. 1:139-146(1975).  
 CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 CC REGION OF THE KAPPA CHAIN REI.  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR: A01862; KIHUAA.  
 DR HSSP: P01607; IREI.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E56F6FB9 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 8.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASNLES 7  
 DB 51 ASNLES 56

RESULT 13  
 KV3V\_MOUSE  
 ID KV3V\_MOUSE STANDARD; PRT; 108 AA.  
 AC P01674;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 2154.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 PIR: A01940; KVM54.  
 DR HSSP: P80362; LWTL.  
 DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGv; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 108  
 FT DISULFID 23 92  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11699 MW; D40921D18DAC4B9E CRC64;

Query Match 87.1%; Score 27; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 8.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASNLES 7  
 DB 55 ASNLES 60

RESULT 14  
 KV3H\_MOUSE  
 ID KV3H\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01660;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region PC 3741/TEPC 111.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (PC 3741).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 PIR: A01934; KVM537.  
 DR HSSP: P01679; 2FBJ.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGv; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 8.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASNLES 7  
 Db 55 ASNLES 60

## RESULT 15

KV3J\_MOUSE  
 ID KV3J\_MOUSE STANDARD; PRT: 111 AA.  
 AC P01662;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-III region ABPC 22/PC 9245.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (ABPC 22).  
 RX MEDLINE=79012520; PubMed=99744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 RT related mouse kappa variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 RN [2]  
 RP SEQUENCE (PC 9245).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity.";  
 RL Nature 276:785-790(1978).  
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01935; KVM5M6.  
 DR HSP: P01679; 2FEJ.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 87.1%; Score 27; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 8.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASNLES 7  
 Db 55 ASNLES 60

Search completed: February 14, 2003, 11:16:23  
 Job time : 4.6129 secs



| Result No. | Score | Query % |      | Length | DB     | ID | Description         |
|------------|-------|---------|------|--------|--------|----|---------------------|
|            |       | Match   |      |        |        |    |                     |
| 1          | 31    | 100.0   | 508  | 4      | Q96RS9 |    | Q96rs9 homo sapien  |
| 2          | 31    | 100.0   | 942  | 3      | Q42938 |    | Q42938 schizosacch  |
| 3          | 31    | 100.0   | 1208 | 4      | Q75162 |    | Q75162 homo sapien  |
| 4          | 28    | 90.3    | 69   | 16     | Q8YFL0 |    | Q8yfl0 brucella me  |
| 5          | 28    | 90.3    | 103  | 11     | Q9JL80 |    | Q9j180 mus musculus |
| 6          | 28    | 90.3    | 204  | 5      | Q9U2Y4 |    | Q9u2y4 caenorhabdi  |
| 7          | 28    | 90.3    | 209  | 16     | Q9A598 |    | Q9a698 caulobacter  |
| 8          | 28    | 90.3    | 228  | 16     | Q8U760 |    | Q8u760 agrobacteri  |
| 9          | 28    | 90.3    | 302  | 10     | Q9A7D5 |    | Q9atd5 gossypium h  |
| 10         | 28    | 90.3    | 579  | 16     | Q8YSM1 |    | Q8yswl anabaena sp  |
| 11         | 28    | 90.3    | 784  | 5      | Q961H5 |    | Q961h5 drosophila   |
| 12         | 27    | 87.1    | 111  | 11     | Q920E9 |    | Q920e9 mus musculus |
| 13         | 27    | 87.1    | 310  | 16     | P94981 |    | P94981 mycobacteri  |
| 14         | 27    | 87.1    | 326  | 16     | Q8YEF7 |    | Q8yef7 brucella me  |
| 15         | 27    | 87.1    | 389  | 10     | Q9SAF7 |    | Q9saf7 arabidopsis  |
| 16         | 27    | 87.1    | 419  | 10     | Q9M887 |    | Q9m887 arabidopsis  |

GN SPBC16H5.02.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=972;  
 RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-  
 CC FRUCTOSE 1,6-BISPHOSPHATE.  
 CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.  
 CC -1- SUBUNIT: HETEROCTAMER OF 4 ALPHA AND 4 BETA CHAINS (BY  
 CC SIMILARITY).  
 DR EMBL; AL022104; CAA17900.1; -.  
 DR HSSP; P00512; 3PFK.  
 DR InterPro; IPR000023; Ppfuckinase.  
 DR Pfam; PF00365; PFK; 2.  
 DR PRINTS; PR00476; PHFRCTKINASE.  
 DR ProDom; PD000707; Ppfuckinase; 2.  
 DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.  
 KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;  
 KW Phosphorylation; Magnesium.  
 SQ SEQUENCE 942 AA; 102554 MW; C6052AF7C1DB75B4 CRC64;

Query Match 100.0%; Score 31; DB 3; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 DB 165 AASNLES 171

## RESULT 3

ID O75162 PRELIMINARY; PRT; 1208 AA.  
 AC O75162;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE KIAA0675 protein.  
 GN KIAA0675.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. X.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 5:169-176(1998).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; AB014575; BAA31650.1; -.  
 DR HSSP; P28990; ICHC.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00184; RING; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 1208 AA; 138604 MW; 76945A63AF85207E CRC64;

Query Match 100.0%; Score 31; DB 4; Length 1208;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AASNLES 7

DB 896 AASNLES 902  
 |||||

## RESULT 4

Q8YFLO PRELIMINARY; PRT; 69 AA.  
 ID Q8YFLO;  
 AC Q8YFLO;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Cold shock protein CSPA.  
 GN BME1510.  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;  
 RX MEDLINE=20020109; PubMed=11756688;  
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujar C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,  
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,  
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyrpides N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 RT Brucella melitensis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 DR EMBL; AE009587; AAL52691.1; -.  
 DR InterPro; IPR002059; Cold\_shock.  
 DR Pfam; PF00313; CSD; 1.  
 DR PRINTS; PR00050; COLDSHOCK.  
 DR ProDom; PD000621; Cold\_shock; 1.  
 DR SMART; SM00357; CSP; 1.  
 DR PROSITE; PS00352; COLD\_SHOCK; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 69 AA; 7301 MW; D6142414631FEDEBA CRC64;

Query Match 90.3%; Score 28; DB 16; Length 69;  
 Best Local Similarity 85.7%; Pred. No. 16;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7  
 DB 62 AASNLES 68  
 |||||

## RESULT 5

ID Q9JL80 PRELIMINARY; PRT; 103 AA.  
 AC Q9JL80;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Anti-myosin immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=20448942; PubMed=10992488;  
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
 RT "T-cell-dependent antibody response to the dominant epitope of  
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive  
 RT with cardiac myosin."  
 RL Infect. Immun. 68:5803-5808(2000).  
 DR EMBL; AF206026; AAF69324.1; -.  
 DR HSSP; P80362; LWTL.  
 DR InterPro; IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Iq\_v.

DR Pfam: PF00047; Iq; 1.

DR SMART: SM00406; IGV; 1.

FT NON\_TER 103

FT NON\_TER 103

SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 90.3%; Score 28; DB 11; Length 103;

Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 46 AASNLES 52

RESULT 6

Q902Y4

Q902Y4 PRELIMINARY; PRT; 204 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE Y113G7A.14 protein.

GN Y113G7A.14

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RP SEQUENCE FROM N.A.

RA Lennard N.

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigative biology";

RL Science 282:2012-2018(1998).

RL EMBL; AL132858; CAB60484.1; -.

SQ SEQUENCE 204 AA; 23067 MW; 8968065DF2EA9C7E CRC64;

Query Match 90.3%; Score 28; DB 5; Length 204;

Best Local Similarity 85.7%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 134 AASNLES 140

RESULT 7

Q9A698

Q9A698 PRELIMINARY; PRT; 209 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Hypothetical protein CC2196.

GN CC2196.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI\_TaxID=155892;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of *Caulobacter crescentus*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
DR EMBL; AE005891; AAK24167.1; -.  
DR TIGR; CC2196; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 209 AA; 22181 MW; D0200247FF7E9E2D CRC64;

Query Match 90.3%; Score 28; DB 16; Length 209;

Best Local Similarity 85.7%; Pred. No. 53;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 151 AASNLES 157

RESULT 8

Q8U760

Q8U760 PRELIMINARY; PRT; 228 AA.

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Hypothetical protein Atu4594.

GN ATU4594 OR AGR.L.563.

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI\_TaxID=176299;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608550; PubMed=11743193;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

RA Kutayin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Nester E.W.;

RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*

C58.";

RL Science 294:2317-2323(2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608551; PubMed=11743194;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,

RA Cielo C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent

*Agrobacterium tumefaciens* C58.";

RL Science 294:2323-2328(2001).

DR EMBL; AE009387; AAL45388.1; -.

DR EMBL; AE008228; AAK88851.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 228 AA; 24816 MW; 4B03E65F8F8A998 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 228;

Best Local Similarity 85.7%; Pred. No. 58;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLES 7

DB 156 AASNLES 162

## RESULT 9

Q9ATD5  
ID Q9ATD5 PRELIMINARY; PRT; 302 AA.  
AC Q9ATD5;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE GHVYB10.  
GN GHVYB10.  
OS Gossypium hirsutum (Upland cotton).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Gossypium.  
OX NCBI\_TaxID=3635;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ACALA MAXXA; TISSUE=DAY OF ANTHESIS OVULE;  
RA Matz E.C., Burr B.;  
RT "Cotton seed fibers are trichomes."  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RM -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
RN -!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.  
DR EMBL; AF336282; AAK19615.1; -;  
DR HSP; P06876; 1MBK.  
DR InterPro; IPR001005; Myb\_DNA\_binding.  
DR Pfam; PF00249; myb\_DNA-binding; 2.  
DR SMART; SM00395; SANT; 2.  
DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
DR PROSITE; PS00334; MYB\_2; 1.  
DR PROSITE; PS00090; MYB\_3; 2.  
KW DNA-binding; Nuclear protein.  
SQ SEQUENCE 302 AA; 33816 MW; 48EE5D9D921ED2D7 CRC64;

Query Match 90.3%; Score 28; DB 10; Length 302;  
Best Local Similarity 85.7%; Pred. No. 79;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7

Db 286 AASNLQS 292

## RESULT 10

Q8YSW1  
ID Q8YSW1 PRELIMINARY; PRT; 579 AA.  
AC Q8YSW1;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical protein All2969.  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."  
RL DNA Res. 8:205-213(2001).  
DR EMBL; AP003591; BAB74668.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 579 AA; 66557 MW; 5C00EBD8CF31BB97 CRC64;

Query Match 90.3%; Score 28; DB 16; Length 579;  
Best Local Similarity 85.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7

Db 378 AASNLDS 384

## RESULT 11

Q961H5  
ID Q961H5 PRELIMINARY; PRT; 784 AA.  
AC Q961H5;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE GH23075P.  
GN KLP68D OR CG7293.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
Yu C., Lewis S.E., Rubin G.M., Celnik S.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY051583; AAK93007.1; -;  
DR FlyBase; FBgn0004381; Klp68D.  
DR InterPro; IPR001752; kinesin\_motor.  
DR Pfam; PF00225; kinesin; 1.  
DR PROSITE; PS00411; KINESIN\_MOTOR\_DOMAIN1; UNKNOWN\_1.  
DR PROSITE; PS00067; KINESIN\_MOTOR\_DOMAIN2; 1.  
KW ATP-binding; Coiled coil; Microtubules; Motor protein.  
SQ SEQUENCE 784 AA; 88207 MW; 7A3C6716D22BC05D CRC64;

Query Match 90.3%; Score 28; DB 5; Length 784;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNL5 7

Db 751 AASNLDS 757

## RESULT 12

Q920E9  
ID Q920E9 PRELIMINARY; PRT; 111 AA.  
AC Q920E9;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Pterin-mimicking anti-idiotope kappa chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307935; AAL09419.1; -;  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 1.  
KW NON\_TER 1  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 12046 MW; 1B46988AA6858526 CRC64;



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Query Match      87.1%; Score 27; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7
DB 55 ASNLES 60

RESULT 13
P94981 ID P94981 PRELIMINARY; PRT; 310 AA.
AC P94981;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 30.2 kDa protein (PE family protein).
RV1646 OR MTCY06H11.11 OR MT1684.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacterium.
OC NCBI_TaxID=1773;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
DR EMBL; 285982; CAB06640.1; -.
DR EMBL; AE007031; AAK45953.1; -.
DR TIGR; MT1684; -.
DR TubercuList; Rv1646; -.
DR InterPro; IPR000084; PE_region.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 310 AA; 30219 MW; F51DFE4CC2D9EDAD CRC64;

Query Match      87.1%; Score 27; DB 16; Length 310;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AASNLES 7
DB 14 AAGNLES 20

RESULT 14
O8YEF7 ID O8YEF7 PRELIMINARY; PRT; 326 AA.
AC O8YEF7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acetoacetyl-CoA synthetase (EC 6.2.1.16).
GN BME11921.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009625; AAL53102.1; -.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 326 AA; 36286 MW; 2092FC153E63A80C CRC64;

Query Match      87.1%; Score 27; DB 16; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASNLE 6
DB 25 AASNLE 30

RESULT 15
Q9SAF7 ID Q9SAF7 PRELIMINARY; PRT; 389 AA.
AC Q9SAF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE F3F19.26 protein.
GN F3F19.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Lenz C.,
RA Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,
RA Altati H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Huiwar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007357; AAD31076.1; -.
DR InterPro; IPR001360; GH_1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR; 8.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 7.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
SQ SEQUENCE 389 AA; 43216 MW; 1DC342A0BF4B7EBF CRC64;

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Query Match 87.1%; Score 27; DB 10; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASNLES 7  
 |  
 |  
 |  
 |  
 |  
 |  
 Db 106 ASNLES 111

Search completed: February 14, 2003, 11:18:43  
 Job time : 16.7312 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:04:17 ; Search time 24.3871 Seconds  
(without alignments)  
49.176 Million cell updates/sec

Title: US-09-701-001B-6  
Perfect score: 48  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 48    | 100.0       | 9      | 21 | AAV59261    |
| 2          | 48    | 100.0       | 9      | 21 | AAV51138    |
| 3          | 48    | 100.0       | 103    | 21 | AAV59263    |
| 4          | 48    | 100.0       | 103    | 21 | AAV51140    |
| 5          | 48    | 100.0       | 111    | 21 | AAV59267    |
| 6          | 48    | 100.0       | 111    | 21 | AAV51144    |
| 7          | 48    | 100.0       | 111    | 21 | AAV51146    |
| 8          | 48    | 100.0       | 131    | 14 | AAK32123    |
| 9          | 48    | 100.0       | 305    | 21 | AAV59264    |
| 10         | 48    | 100.0       | 305    | 21 | AAV59265    |

|    |    |       |     |    |          |                    |
|----|----|-------|-----|----|----------|--------------------|
| 11 | 48 | 100.0 | 305 | 21 | AAV51141 | Murine derived pro |
| 12 | 48 | 100.0 | 305 | 21 | AAV51142 | Murine derived pro |
| 13 | 45 | 93.8  | 9   | 16 | AAV70197 | MAB 3B9 light chai |
| 14 | 45 | 93.8  | 9   | 20 | AAV23774 | CDR of the light c |
| 15 | 45 | 93.8  | 9   | 20 | AAV18116 | Light chain CDR fo |
| 16 | 45 | 93.8  | 111 | 20 | AAV23781 | Light chain variab |
| 17 | 45 | 93.8  | 111 | 20 | AAV18123 | Light chain sequen |
| 18 | 45 | 93.8  | 131 | 13 | AAV29008 | p64-k4 protein pro |
| 19 | 45 | 93.8  | 131 | 16 | AAV70202 | Humanized antibody |
| 20 | 45 | 93.8  | 131 | 18 | AAW30274 | Light chain of Hum |
| 21 | 45 | 93.8  | 131 | 18 | AAW30278 | Light chain of Mum |
| 22 | 45 | 93.8  | 131 | 20 | AAV23779 | Light chain variab |
| 23 | 45 | 93.8  | 131 | 20 | AAV18126 | Light chain sequen |
| 24 | 45 | 93.8  | 132 | 16 | AAV70189 | Mouse MAB 3B9 ligh |
| 25 | 45 | 93.8  | 132 | 20 | AAV23767 | Light chain variab |
| 26 | 45 | 93.8  | 132 | 20 | AAV18120 | Light chain sequen |
| 27 | 42 | 87.5  | 17  | 15 | AAK66145 | CD-4 antibody vari |
| 28 | 42 | 87.5  | 115 | 11 | AAK04134 | Anti-Leu 3a light  |
| 29 | 42 | 87.5  | 131 | 11 | AAK04132 | Anti-Leu 3a light  |
| 30 | 40 | 83.3  | 9   | 16 | AAV70201 | Humanized antibody |
| 31 | 40 | 83.3  | 9   | 20 | AAV23778 | CDR of the light c |
| 32 | 40 | 83.3  | 9   | 20 | AAV18119 | Light chain CDR fo |
| 33 | 40 | 83.3  | 10  | 23 | AAU70354 | Mouse kappa III li |
| 34 | 40 | 83.3  | 131 | 16 | AAV75355 | Humanized antibody |
| 35 | 40 | 83.3  | 131 | 20 | AAV23771 | Light chain variab |
| 36 | 40 | 83.3  | 131 | 20 | AAV18118 | Light chain sequen |
| 37 | 38 | 79.2  | 282 | 21 | AAK41486 | Arabidopsis thalia |
| 38 | 38 | 79.2  | 301 | 21 | AAK41485 | Arabidopsis thalia |
| 39 | 38 | 79.2  | 304 | 22 | AAE02541 | A. thaliana transc |
| 40 | 38 | 79.2  | 304 | 23 | AAU92994 | Arabidopsis transc |
| 41 | 38 | 79.2  | 318 | 21 | AAK41484 | Arabidopsis thalia |
| 42 | 37 | 77.1  | 215 | 16 | AAK64202 | Monoclonal antibod |
| 43 | 37 | 77.1  | 495 | 21 | AAK29957 | Arabidopsis thalia |
| 44 | 37 | 77.1  | 513 | 21 | AAK29956 | Arabidopsis thalia |
| 45 | 37 | 77.1  | 517 | 21 | AAK29955 | Arabidopsis thalia |

## ALIGNMENTS

RESULT 1  
AAV59261  
ID AAV59261 standard; peptide; 9 AA.  
XX AAV59261;  
XX  
XX  
XX  
DT 17-APR-2000 (first entry)  
XX  
DE Antibody 4H5 L chain variable region CDR3 fragment.  
DE  
KW CD4 antigen; anti-human; antibody; 4H5; drug; CDR;  
KW complementarity determining region.  
XX  
OS Mus sp.  
XX  
XX JP11332563-A.  
XX  
PD 07-DEC-1999.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX 26-MAY-1998; 98JP-0163034.  
XX  
XX (ASAH ) ASAH KASEI KOGYO KK.  
XX  
DR WPI; 2000-091351/08.  
XX  
PT An antibody and the nucleic acid coding the antibody -  
XX  
XX  
PS Claim 2; Page 14; 25pp; Japanese.  
XX  
XX The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC

CC application for drugs. It is highly safe in human dose. Sequences  
CC AAY59259-61 represent the complementarity determining region (CDR)-1,  
CC CDR-2 and CDR-3 fragments in the L chain variable region of the  
CC antibody 4H5 respectively.  
XX  
SQ Sequence 9 AA;  
  
Query Match 100.0%; Score 48; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QOSSEDPPT 9  
| | | | | | | | | |  
Db 1 QOSSEDPPT 9  
  
RESULT 2  
AAY51138  
ID AAY51138 standard; Protein; 9 AA.  
XX  
AC AAY51138;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Murine CD4/CD34 recognizing antibody light chain CDR-3 region #1.  
XX  
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; complementarity determining region;  
KW CDR-3; light chain; murine.  
XX  
OS Mus sp.  
XX  
PN WO9961629-A1.  
XX  
PD 02-DEC-1999.  
XX  
PF 24-MAY-1999; 99WO-JP02711.  
XX  
PR 25-MAY-1998; 98JP-0159957.  
XX  
PR 26-MAY-1998; 98JP-0163023.  
XX  
XX (ASAH ) ASAH KASEI KOGYO KK.  
PA (ASAH ) ASAH MEDICAL CO LTD.  
PI Ono M, Soka T, Morimoto I, Miyamura K;  
XX WPI; 2000-086720/07.  
XX  
XX Devices containing antibodies recognising CD4 or CD34 and their use for  
XX the separation of CD4 or CD34 positive cells -  
XX  
PS Claim 3; Page 77; 111pp; Japanese.  
XX  
XX This invention describes a novel device (I) for separating cluster  
CC differentiation (CD)-positive cells using a recombinant (Chimeric or  
CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
CC for the separation of CD4 or CD34 positive cells, which is useful for  
CC the collection of hematopoietic undifferentiated cells, elimination of  
CC lymphocytes from cells to be used in bone marrow transplantation, the  
CC detection of leukemic cells and the production of medicinal  
CC compositions for the treatment of HIV infection and autoimmune diseases.  
CC This sequence represents a murine derived complementarity determining  
CC region CDR-3 protein fragment which is used to illustrate the method of  
CC the invention.  
XX  
SQ Sequence 9 AA;  
  
Query Match 100.0%; Score 48; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QOSSEDPPT 9  
| | | | | | | | | |  
Db 1 QOSSEDPPT 9

Db 1 QOSSEDPPT 9  
| | | | | | | | | |  
RESULT 3  
AAY59263  
ID AAY59263 standard; protein; 103 AA.  
XX  
AC AAY59263;  
XX  
DT 17-APR-2000 (first entry)  
XX  
DE Antibody 4H5 L chain variable region.  
XX  
KW CD4 antigen; anti-human; antibody; 4H5; drug.  
XX  
OS Mus sp.  
XX  
PN JP11332563-A.  
XX  
PD 07-DEC-1999.  
XX  
PF 26-MAY-1998; 98JP-0163034.  
XX  
PR 26-MAY-1998; 98JP-0163034.  
XX  
PA (ASAH ) ASAH KASEI KOGYO KK.  
XX  
XX WPI; 2000-091351/08.  
DR N-PSDB; AAZ58662.  
XX  
XX An antibody and the nucleic acid coding the antibody -  
XX  
XX Claim 5; Page 15-16; 25pp; Japanese.  
XX  
XX The invention provides an antibody having affinity to CD4 antigen. The  
CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
CC application for drugs. It is highly safe in human dose. The present  
CC sequence represents the L chain variable region of the antibody 4H5.  
XX  
SQ Sequence 103 AA;  
  
Query Match 100.0%; Score 48; DB 21; Length 103;  
Best Local Similarity 100.0%; Pred. No. 0.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QOSSEDPPT 9  
| | | | | | | | | |  
Db 85 QOSSEDPPT 93  
  
RESULT 4  
AAY51140  
ID AAY51140 standard; Protein; 103 AA.  
XX  
AC AAY51140;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Murine derived protein fragment #2.  
XX  
KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
KW HIV infection; autoimmune disease; murine.  
XX  
OS Mus sp.  
XX  
PN WO9961629-A1.  
XX  
PD 02-DEC-1999.  
XX  
PF 24-MAY-1999; 99WO-JP02711.  
XX

PR 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 XX  
 XX (ASAH ) ASAHI KASEI KOGYO KK.  
 XX (ASAH ) ASAHI MEDICAL CO LTD.  
 XX  
 XX PI Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI; 2000-086720/07.  
 DR N-PSDB; AAZ44204.  
 XX  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 XX Claim 22; Page 79; 111pp; Japanese.  
 XX  
 XX This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 XX SQ Sequence 103 AA;

Query Match 100.0%; Score 48; DB 21; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 0.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSSEDPPT 9  
 Db 85 QOSSEDPPT 93

RESULT 5  
 AAY59267  
 ID AAY59267 standard; protein; 111 AA.  
 XX  
 XX AC AAY59267;  
 XX  
 XX 17-APR-2000 (first entry)  
 DT  
 XX Antibody 4H5 L chain fragment.  
 XX  
 XX CD4 antigen; anti-human; antibody; 4H5; drug.  
 KW  
 XX Mus sp.  
 OS  
 XX JP11332563-A.  
 PN  
 XX 07-DEC-1999.  
 PD  
 XX 26-MAY-1998; 98JP-0163034.  
 PF  
 XX 26-MAY-1998; 98JP-0163034.  
 PR  
 XX (ASAH ) ASAHI KASEI KOGYO KK.  
 XX  
 XX WPI; 2000-091351/08.  
 DR N-PSDB; AAZ58690.  
 DR  
 XX An antibody and the nucleic acid coding the antibody -  
 PT  
 XX Disclosure; Page 22-23; 25pp; Japanese.  
 PS  
 XX The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents a L chain fragment of the antibody 4H5.

XX SQ Sequence 111 AA;  
 Query Match 100.0%; Score 48; DB 21; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSSEDPPT 9  
 Db 93 QOSSEDPPT 101

RESULT 6  
 AAY51144  
 ID AAY51144 standard; Protein; 111 AA.  
 XX  
 XX AC AAY51144;  
 XX  
 XX 31-MAR-2000 (first entry)  
 DT  
 XX Murine derived protein fragment #6.  
 DE  
 XX Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX  
 XX Mus sp.  
 OS  
 XX WO9961629-A1.  
 PN  
 XX 02-DEC-1999.  
 PD  
 XX 24-MAY-1999; 99WO-JP02711.  
 PF  
 XX 25-MAY-1998; 98JP-0159957.  
 PR  
 XX 26-MAY-1998; 98JP-0163023.  
 PR  
 XX (ASAH ) ASAHI KASEI KOGYO KK.  
 PA (ASAH ) ASAHI MEDICAL CO LTD.  
 PA  
 XX Ono M, Soka T, Morimoto I, Miyamura K;  
 PI WPI; 2000-086720/07.  
 DR  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 XX Disclosure; Page 95; 111pp; Japanese.  
 PS  
 XX This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 XX SQ Sequence 111 AA;  
 Query Match 100.0%; Score 48; DB 21; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QOSSEDPPT 9  
 Db 93 QOSSEDPPT 101

RESULT 7  
 AAY51146

ID AAY51146 standard; Protein; 111 AA.  
 XX AAY51146;  
 AC  
 XX  
 DT 31-MAR-2000 (first entry)  
 XX  
 XX Murine derived protein fragment #8.  
 DE  
 DE Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.  
 XX  
 OS Mus sp.  
 XX  
 XX WO9961629-A1.  
 PN  
 XX  
 XX  
 PD 02-DEC-1999.  
 XX  
 XX 24-MAY-1999; 99WO-JP02711.  
 PF  
 XX  
 PR 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 XX  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 XX Ono M, Soka T, Morimoto I, Miyamura K;  
 PI  
 XX  
 XX WPI: 2000-086720/07.  
 DR N-PSDB; AA244232.  
 XX  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells  
 PT  
 XX  
 XX Disclosure; Page 97-98; 111pp; Japanese.  
 PS  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD) positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 XX Sequence 111 AA;  
 SQ  
 Query Match 100.0%; Score 48; DB 21; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQSSEDPPT 9  
 DB 93 QQSSEDPPT 101  
 RESULT 8  
 AAR32123  
 ID AAR32123 standard; Protein; 131 AA.  
 XX  
 AC AAR32123;  
 XX  
 DT 02-JUN-1993 (first entry)  
 XX  
 XX Anti-CD4 antibody MT 3.10 light chain variable region.  
 DE  
 XX immunosuppression; tissue transplantation; graft; L chain; V region;  
 KW T-helper cell inhibition; transplant rejection; MAB;  
 KW interleukin-2 receptor.  
 XX  
 FH Key Location/Qualifiers

FT Peptide 1..20  
 FT /label= signal  
 FT Region 21..120  
 FT /label= Variable  
 FT Region 121..131  
 FT /label= J1  
 XX  
 PN DE4143214-A.  
 XX  
 PD 28-JAN-1993.  
 XX  
 PF 30-DEC-1991; 91DE-4143214.  
 XX  
 PR 25-JUL-1991; 91DE-4124759.  
 PR 30-DEC-1991; 91DE-4143214.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Kaluza B, Riethmuller G, Scheuer W, Weidie U;  
 XX  
 DR WPI: 1993-037582/05.  
 DR N-PSDB; AAQ36609.  
 XX  
 XX Synergistic antibody compsn. for use as immunosuppressant -  
 PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R  
 PT alpha- or anti-IL2R beta antibodies  
 XX  
 PS Claim 5; Page 11; 18pp; German.  
 XX  
 CC This sequence is the light chain variable region of a preferred  
 CC anti-CD4 monoclonal antibody for use in the claimed synergistic  
 CC composition. MAB MT 3.10 is deposited as clone 3.101/SB10 (ECACC  
 CC 9090702). The anti-CD4 antibody is used with at least one anti-IL2R  
 CC alpha or beta antibody. Individually the antibodies are strongly  
 CC inhibiting and when used together they immunosuppressive properties  
 CC are improved; they synergistically inhibit T-helper cell  
 CC proliferation to effectively inhibit transplant rejection at low  
 CC doses without significantly reducing the general immune response.  
 CC See also AAQ36608-Q36616.  
 XX  
 SQ Sequence 131 AA;  
 Query Match 100.0%; Score 48; DB 14; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 0.76;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQSSEDPPT 9  
 DB 113 QQSSEDPPT 121  
 RESULT 9  
 AAY59264  
 ID AAY59264 standard; protein; 305 AA.  
 XX  
 AC AAY59264;  
 XX  
 DT 17-APR-2000 (first entry)  
 XX  
 DE Antibody 4H5 H chain sequence.  
 XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.  
 XX  
 OS Mus sp.  
 XX  
 PN JP11332563-A.  
 XX  
 PD 07-DEC-1999.  
 XX  
 PF 26-MAY-1998; 98JP-0163034.  
 XX  
 PR 26-MAY-1998; 98JP-0163034.  
 XX

PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX  
 DR WPI; 2000-091351/08.  
 DR N-PSDB; AA258663.

PT An antibody and the nucleic acid coding the antibody -

XX  
 XX  
 PS Disclosure; Page 16-17; 25pp; Japanese.

XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the H chain sequence of the antibody 4H5.

XX  
 XX  
 SQ Sequence 305 AA;

Query Match 100.0%; Score 48; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 115 QOSSEDPPT 123

RESULT 10

AA59265  
 ID AAY59265 standard; protein; 305 AA.

XX  
 AC AAY59265;

XX  
 DT 17-APR-2000 (first entry)

XX  
 DE Antibody 4H5 L chain sequence.

XX  
 KW CD4 antigen; anti-human; antibody; 4H5; drug.

XX  
 OS Mus sp.

XX  
 PN JP11332563-A.

XX  
 PD 07-DEC-1999.

XX  
 PF 26-MAY-1998; 98JP-0163034.

XX  
 PR 26-MAY-1998; 98JP-0163034.

XX  
 (ASAH ) ASahi KASEI KOGYO KK.

XX  
 WPI; 2000-091351/08.

XX  
 DR N-PSDB; AA258664.

XX  
 PT An antibody and the nucleic acid coding the antibody -

XX  
 PS Disclosure; Page 17-18; 25pp; Japanese.

XX  
 CC The invention provides an antibody having affinity to CD4 antigen. The  
 CC anti-human CD4 antibody 4H5 is used for the detection of antigen and  
 CC application for drugs. It is highly safe in human dose. The present  
 CC sequence represents the L chain sequence of the antibody 4H5.

XX  
 SQ Sequence 305 AA;

Query Match 100.0%; Score 48; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 248 QOSSEDPPT 256

RESULT 11

AA51141  
 ID AAY51141 standard; Protein; 305 AA.  
 XX  
 AC AAY51141;

XX  
 DT 31-MAR-2000 (first entry)

XX  
 DE Murine derived protein fragment #3.

XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.

OS Mus sp.

XX  
 PN WO9961629-A1.

XX  
 PD 02-DEC-1999.

XX  
 PF 24-MAY-1999; 99WO-JP02711.

XX  
 PR 25-MAY-1998; 98JP-0159957.

XX  
 PR 26-MAY-1998; 98JP-0163023.

XX  
 PA (ASAH ) ASahi KASEI KOGYO KK.

XX  
 PA (ASAH ) ASahi MEDICAL CO LTD.

XX  
 PI Ono M, Soka T, Morimoto I, Miyamura K;

XX  
 WPI; 2000-086720/07.

XX  
 DR N-PSDB; AA244205.

XX  
 PT Devices containing antibodies recognising CD4 or CD34 and their use for  
 the separation of CD4 or CD34 positive cells

XX  
 PS Claim 22; Page 80-82; 11pp; Japanese.

XX  
 CC This invention describes a novel device (I) for separating cluster  
 differentiation (CD)-positive cells using a recombinant (chimeric or  
 single-chain) antibody recognising CD4 or CD34. The devices are useful  
 for the separation of CD4 or CD34 positive cells, which is useful for  
 the collection of hematopoietic undifferentiated cells, elimination of  
 lymphocytes from cells to be used in bone marrow transplantation, the  
 detection of leukemic cells and the production of medicinal  
 compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 to illustrate the method of the invention.

XX  
 SQ Sequence 305 AA;

Query Match 100.0%; Score 48; DB 21; Length 305;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

DB 115 QOSSEDPPT 123

RESULT 12

AA51142

ID AAY51142 standard; Protein; 305 AA.

XX  
 AC AAY51142;

XX  
 DT 31-MAR-2000 (first entry)

XX  
 DE Murine derived protein fragment #4.

XX  
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;  
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;  
 KW HIV infection; autoimmune disease; murine.

OS Mus sp.  
 PN WO9961629-A1.  
 XX  
 XX  
 PD 02-DEC-1999.  
 XX  
 XX 24-MAY-1999; 99WO-JP02711.  
 XX  
 XX 25-MAY-1998; 98JP-0159957.  
 PR 26-MAY-1998; 98JP-0163023.  
 XX  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 PA (ASAH ) ASAH MEDICAL CO LTD.  
 XX  
 XX Ono M, Soka T, Morimoto I, Miyamura K;  
 XX WPI: 2000-086720/07.  
 DR N-PSDB; AAZ44206.  
 XX  
 XX Devices containing antibodies recognising CD4 or CD34 and their use for  
 PT the separation of CD4 or CD34 positive cells -  
 XX  
 XX Claim 22; Page 82-84; 111pp; Japanese.  
 XX  
 CC This invention describes a novel device (I) for separating cluster  
 CC differentiation (CD)-positive cells using a recombinant (chimeric or  
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful  
 CC for the separation of CD4 or CD34 positive cells, which is useful for  
 CC the collection of hematopoietic undifferentiated cells, elimination of  
 CC lymphocytes from cells to be used in bone marrow transplantation, the  
 CC detection of leukemic cells and the production of medicinal  
 CC compositions for the treatment of HIV infection and autoimmune diseases.  
 CC This sequence represents a murine derived protein fragment which is used  
 CC to illustrate the method of the invention.  
 XX  
 XX Sequence 305 AA;  
 SQ  
 Query Match 100.0%; Score 48; DB 21; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQSSEDPPT 9  
 Db 248 QQSSEDPPT 256  
 |||:|||||  
 RESULT 13  
 AAR70197  
 ID AAR70197 standard; Protein; 9 AA.  
 XX  
 XX AAR70197;  
 DT 20-SEP-1995 (first entry)  
 XX  
 XX Mab 3B9 light chain CDR.  
 DE  
 XX  
 XX Chimeric antibody; humanized antibody; antibody engineering;  
 KW monoclonal antibody; Mab; interleukin-4; IL-4; allergy; CDR;  
 KW complementarity determining region.  
 XX  
 XX Mus sp.  
 OS  
 XX  
 XX WO9507301-A.  
 PN  
 XX  
 XX 16-MAR-1995.  
 PD  
 XX  
 XX 07-SEP-1994; 94WO-US10308.  
 PF  
 XX  
 XX 07-SEP-1993; 93US-0117366.  
 PR  
 XX 14-OCT-1993; 93US-0136783.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX

XX Gross MS, Holmes SD, Sylvester DR;  
 PI WPI: 1995-123387/16.  
 XX  
 XX Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived  
 PT from high affinity mAbs - useful in treatment of IL-4-mediated  
 PT and IgE-mediated allergic conditions  
 XX  
 XX Disclosure; Page 56; 97pp; English.  
 XX  
 CC Spleen cells from mice immunized with human IL-4 were used to prepare  
 CC hybridomas, which were screened for anti-IL-4 Mab secretion. Only  
 CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy  
 CC chains were cloned into pGEM7i+ and transformed into E. coli  
 CC DH5-alpha. A light chain cDNA clone was sequenced (AAQ83490) that  
 CC encoded the protein given in AAR70189. 3 CDRs (AAR70195-97) were  
 CC identified.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 93.8%; Score 45; DB 16; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QQSSEDPPT 9  
 |||:|||||  
 Db 1 QQSSEDPPT 9  
 RESULT 14  
 AAY23774  
 ID AAY23774 standard; Peptide; 9 AA.  
 XX  
 XX AAY23774;  
 AC  
 XX  
 XX 13-SEP-1999 (first entry)  
 DT  
 XX  
 XX CDR of the light chain variable region of antibody 3B9.  
 DE  
 XX  
 XX Light chain variable region; interleukin-4; IL-4; antibody 3B9;  
 KW chimeric antibody; humanised antibody; IL-4 mediated allergic reaction;  
 KW immunoglobulin E-mediated allergic reaction; allergic rhinitis;  
 KW conjunctivitis; atopic dermatitis; atopic asthma; anaphylactic shock;  
 KW rheumatoid arthritis; host-versus-graft disease; renal disease;  
 KW allergy; complementarity determining region.  
 XX  
 XX Mus sp.  
 OS  
 XX  
 XX US5928904-A.  
 PN  
 XX  
 XX 27-JUL-1999.  
 PD  
 XX  
 XX 07-JUN-1995; 95US-0483632.  
 PF  
 XX  
 XX 07-JUN-1995; 95US-0483632.  
 PR  
 XX 07-SEP-1993; 93US-0117366.  
 PR  
 XX 14-OCT-1993; 93US-0136783.  
 PR  
 XX 07-SEP-1994; 94WO-US10308.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Gross MS, Holmes SD, Sylvester DR;  
 PI WPI: 1999-429500/36.  
 DR N-PSDB; AAX85891.  
 XX  
 XX New DNA molecules encoding recombinant antibodies useful for  
 PT treating IL4-mediated conditions  
 XX  
 XX Example 3; Column 45; 50pp; English.  
 PS  
 XX



CC The present sequence represents a complementarity determining region  
 CC (CDR) of the light chain variable region of murine interleukin-4  
 CC (IL-4) antibody 3B9. The specification describes chimeric and  
 CC humanised IL-4 monoclonal antibodies. The antibodies of the  
 CC invention are used in therapeutic and pharmaceutical compositions  
 CC for treating IL-4 mediated and immunoglobulin E-mediated allergic  
 CC reactions e.g. allergic rhinitis, conjunctivitis, atopic dermatitis,  
 CC atopic asthma, anaphylactic shock, rheumatoid arthritis,  
 CC host-versus-graft disease and renal disease. They are also useful  
 CC in the diagnosis of an allergy or condition associated with excess  
 CC IL-4 production through the measurement e.g. by ELISA of circulating  
 CC endogenous IL-4 levels in humans.

XX  
 XX  
 SQ Sequence 9 AA;

Query Match 93.8%; Score 45; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 7.8e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 QQSSEDPPT 9

111:|||||

Db 1 QQSNEPDPT 9

# RESULT 15

AAV18116

ID AAY18116 standard; peptide; 9 AA.

XX AC AAY18116;

XX DT 11-AUG-1999 (first entry)

XX DE Light chain CDR for hIL-4 specific antibody.

XX KW Antibody; interleukin-4; IL4; immunoglobulin E; IgE mediated disease;  
 KW allergic disorder; allergic rhinitis; conjunctivitis; atopic dermatitis;  
 KW atopic asthma; anaphylactic shock; cell proliferation regulator; therapy;  
 KW autoimmune disease; graft versus host disease;  
 KW complementarity determining region; CDR.

XX OS Synthetic.

XX PN US5914110-A.

XX PD 22-JUN-1999.

XX PY 07-JUN-1995; 95US-0483636.

PR 07-JUN-1995; 95US-0483636.

PR 07-SEP-1993; 93US-0117366.

PR 14-OCT-1993; 93US-0136783.

PR 07-SEP-1994; 94WO-US10308.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX PI Gross MS, Holmes SD, Sylvester DR;

XX DR WPI; 1999-370482/31.

XX DR N-PSDE; AAX79515.

XX PT Recombinant IL4 antibodies

XX PS Claim 7; Column 45; 50pp; English.

XX This sequence represents a light chain complementarity determining region  
 CC (CDR) from an antibody of the invention. The antibody is a chimeric or  
 CC humanised interleukin-4 (IL4) monoclonal antibody for the treatment of  
 CC immunoglobulin E (IgE) mediated diseases. The antibodies are useful for  
 CC the treatment of allergic disorders such as allergic rhinitis,  
 CC conjunctivitis, atopic dermatitis, atopic asthma and anaphylactic shock.  
 CC The antibodies are also useful for regulating B and T cell proliferation  
 CC and as such are useful in the treatment of autoimmune diseases and graft

CC versus host disease.

XX

SQ Sequence 9 AA;

Query Match

93.8%; Score 45; DB 20; Length 9;

Best Local Similarity 88.9%; Pred. No. 7.8e+05;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9

111:|||||

Db 1 QQSNEPDPT 9

Search completed: February 14, 2003, 11:15:45

Job time : 24.3871 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:13:07 : Search time 8.12903 Seconds  
(without alignments)  
32.575 Million cell updates/sec

Title: US-09-701-001b-6

Perfect score: 48

Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 45    | 93.8        | 9      | 2     | US-08-483-636-20   |
| 2          | 45    | 93.8        | 9      | 2     | US-08-483-632-20   |
| 3          | 45    | 93.8        | 111    | 2     | US-08-483-636-73   |
| 4          | 45    | 93.8        | 111    | 2     | US-08-483-632-73   |
| 5          | 45    | 93.8        | 131    | 1     | US-08-137-117D-33  |
| 6          | 45    | 93.8        | 131    | 2     | US-08-436-717-33   |
| 7          | 45    | 93.8        | 131    | 2     | US-08-621-751A-10  |
| 8          | 45    | 93.8        | 131    | 2     | US-08-621-751A-14  |
| 9          | 45    | 93.8        | 131    | 2     | US-08-483-636-58   |
| 10         | 45    | 93.8        | 131    | 2     | US-08-483-632-58   |
| 11         | 45    | 93.8        | 132    | 2     | US-08-483-636-2    |
| 12         | 45    | 93.8        | 132    | 2     | US-08-483-632-2    |
| 13         | 40    | 83.3        | 9      | 2     | US-08-483-636-28   |
| 14         | 40    | 83.3        | 9      | 2     | US-08-483-632-28   |
| 15         | 40    | 83.3        | 131    | 2     | US-08-483-636-14   |
| 16         | 40    | 83.3        | 131    | 2     | US-08-483-632-14   |
| 17         | 37    | 77.1        | 9      | 4     | US-09-170-769A-21  |
| 18         | 37    | 77.1        | 215    | 4     | US-09-170-769A-4   |
| 19         | 36    | 75.0        | 15     | 2     | US-08-945-168B-117 |
| 20         | 36    | 75.0        | 412    | 2     | US-08-463-081B-14  |
| 21         | 36    | 75.0        | 412    | 2     | US-08-461-379A-14  |
| 22         | 36    | 75.0        | 412    | 2     | US-08-462-390B-14  |
| 23         | 36    | 75.0        | 412    | 3     | US-08-463-074B-14  |
| 24         | 36    | 75.0        | 412    | 3     | US-08-465-585C-14  |
| 25         | 36    | 75.0        | 412    | 3     | US-08-652-446-14   |
| 26         | 36    | 75.0        | 412    | 4     | US-09-462-624-2    |
| 27         | 35    | 72.9        | 9      | 5     | PCT-US94-14106-42  |

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|----|----|------|-----|---|-------------------|
| 28 | 34 | 70.8 | 9   | 5 | PCT-US94-14106-43 |
| 29 | 34 | 70.8 | 106 | 3 | US-08-466-151-6   |
| 30 | 34 | 70.8 | 106 | 4 | US-08-466-163B-6  |
| 31 | 34 | 70.8 | 111 | 1 | US-08-491-845-8   |
| 32 | 34 | 70.8 | 111 | 1 | US-08-491-845-16  |
| 33 | 34 | 70.8 | 115 | 3 | US-08-513-968-51  |
| 34 | 34 | 70.8 | 131 | 4 | US-08-579-378A-14 |
| 35 | 34 | 70.8 | 131 | 4 | US-08-579-378A-18 |
| 36 | 34 | 70.8 | 218 | 5 | PCT-US96-13152-2  |
| 37 | 33 | 68.8 | 28  | 3 | US-08-984-277-7   |
| 38 | 33 | 68.8 | 111 | 2 | US-08-887-352B-5  |
| 39 | 33 | 68.8 | 111 | 3 | US-08-887-352B-6  |
| 40 | 33 | 68.8 | 111 | 3 | US-08-466-151-2   |
| 41 | 33 | 68.8 | 111 | 4 | US-09-109-207C-5  |
| 42 | 33 | 68.8 | 111 | 4 | US-09-109-207C-6  |
| 43 | 33 | 68.8 | 111 | 4 | US-09-296-005-5   |
| 44 | 33 | 68.8 | 111 | 4 | US-09-296-005-6   |
| 45 | 33 | 68.8 | 111 | 4 | US-08-466-163B-2  |

## ALIGNMENTS

RESULT 1  
US-08-483-636-20  
; Sequence 20, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESS: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

Sequence 43, Appl  
Sequence 6, Appli  
Sequence 8, Appli  
Sequence 16, Appl  
Sequence 51, Appl  
Sequence 14, Appl  
Sequence 18, Appl  
Sequence 2, Appli  
Sequence 7, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 5, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 2, Appli

US-08-483-636-20

Query Match 93.8%; Score 45; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
|:|:|:|:|:|  
Db 1 QOSNEDPPT 9

## RESULT 2

US-08-483-632-20  
; Sequence 20, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483.632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-483-632-20

Query Match 93.8%; Score 45; DB 2; Length 9;  
Best Local Similarity 88.9%; Pred. No. 2e+05;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
|:|:|:|:|:|  
Db 1 QOSNEDPPT 9

## RESULT 3

US-08-483-636-73

; Sequence 73, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483.636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-483-636-73

Query Match 93.8%; Score 45; DB 2; Length 111;  
Best Local Similarity 88.9%; Pred. No. 0.51;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
|:|:|:|:|:|  
Db 93 QOSNEDPPT 101

## RESULT 4

US-08-483-632-73  
; Sequence 73, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Smithkline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-483-632-73

Query Match 93.8%; Score 45; DB 2; Length 111;  
Best Local Similarity 88.9%; Pred. No. 0.51;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
111:111111  
93 QQSNEPDPT 101

RESULT 5  
US-08-137-117D-33  
Sequence 33, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 131 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-33

Query Match 93.8%; Score 45; DB 1; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.6;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
111:111111  
Db 113 QQSNEPDPT 121

RESULT 6  
US-08-436-717-33  
Sequence 33, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544

; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; 8-436-717-33

Query Match 93.8%; Score 45; DB 2; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.6;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
Db 113 QOSNEDPPT 121

RESULT 7  
US-08-621-751A-10  
; Sequence 10, Application US/08621751A  
; Patent No. 5882644  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Chung N.  
; APPLICANT: Landolfi, Nicholas F.  
; APPLICANT: Martin, Ulrich  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER LLP  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/621,751A  
; FILING DATE: 22-MAR-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 321152000100  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX: 706141 MRSN FOERS SFO  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-621-751A-10

Query Match 93.8%; Score 45; DB 2; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.6;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
Db 113 QOSNEDPPT 121

RESULT 8  
US-08-621-751A-14  
; Sequence 14, Application US/08621751A  
; Patent No. 5882644  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Chung N.  
; APPLICANT: Landolfi, Nicholas F.  
; APPLICANT: Martin, Ulrich  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER LLP  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/621,751A  
; FILING DATE: 22-MAR-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K.  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 321152000100  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX: 706141 MRSN FOERS SFO  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-621-751A-14

Query Match 93.8%; Score 45; DB 2; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.6;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
Db 113 QOSNEDPPT 121

RESULT 9  
US-08-483-636-58  
; Sequence 58, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.

;; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
;; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
;; NUMBER OF SEQUENCES: 75  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SmithKline Beecham Corp./Corporate  
;; ADDRESSEE: Intellectual Property  
;; STREET: P.O. Box 1539 / UW2220  
;; CITY: King of Prussia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19406-0939  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/483,636  
;; FILING DATE:  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/117366  
;; FILING DATE: 07-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/136783  
;; FILING DATE: 14-OCT-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US/94/10308  
;; FILING DATE: 07-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50186-3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5024  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 58:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 131 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-483-636-58

Query Match 93.8%; Score 45; DB 2; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.6;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSEDPPT 9  
111:11111  
Db 112 QQSNEDPPT 120

RESULT 10  
US-08-483-632-58  
; Sequence 58, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-483-636-58

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/483,632  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/117366  
;; FILING DATE: 07-SEP-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/136783  
;; FILING DATE: 14-OCT-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US/94/10308  
;; FILING DATE: 07-SEP-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sutton, Jeffrey A.  
;; REGISTRATION NUMBER: 34,028  
;; REFERENCE/DOCKET NUMBER: P50186-3  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 270-5024  
;; TELEFAX: (215) 270-5090  
;; INFORMATION FOR SEQ ID NO: 58:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 131 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-483-632-58

Query Match 93.8%; Score 45; DB 2; Length 131;  
Best Local Similarity 88.9%; Pred. No. 0.6;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSEDPPT 9  
111:11111  
Db 112 QQSNEDPPT 120

RESULT 11  
US-08-483-636-2  
; Sequence 2, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/136783  
 ; FILING DATE: 14-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US/94/10308  
 ; FILING DATE: 07-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P50186-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 270-5024  
 ; TELEFAX: (215) 270-5090  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 132 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-483-636-2

Query Match 93.8%; Score 45; DB 2; Length 132;  
 Best Local Similarity 88.9%; Pred. No. 0.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
 Db 113 QQSNEPPT 121

RESULT 12  
 US-08-483-632-2  
 ; Sequence 2, Application US/08483632  
 ; Patent No. 5928904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holmes, Stephen D.  
 ; APPLICANT: Gross, Mitchell S.  
 ; APPLICANT: Sylvester, Daniel R.  
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 ; TREATMENT OF IL4 Mediated Disorders  
 ; NUMBER OF SEQUENCES: 75  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate  
 ; ADDRESS: Intellectual Property  
 ; STREET: P.O. Box 1539 / UW2220  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/483,632  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/117366  
 ; FILING DATE: 07-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/136783  
 ; FILING DATE: 14-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US/94/10308  
 ; FILING DATE: 07-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P50186-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 270-5024  
 ; TELEFAX: (215) 270-5090

; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 132 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-483-632-2

Query Match 93.8%; Score 45; DB 2; Length 132;  
 Best Local Similarity 88.9%; Pred. No. 0.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
 Db 113 QQSNEPPT 121

RESULT 13  
 US-08-483-636-28  
 ; Sequence 28, Application US/08483636  
 ; Patent No. 5914110  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Holmes, Stephen D.  
 ; APPLICANT: Gross, Mitchell S.  
 ; APPLICANT: Sylvester, Daniel R.  
 ; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
 ; TREATMENT OF IL4 Mediated Disorders  
 ; NUMBER OF SEQUENCES: 75  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate  
 ; ADDRESS: Intellectual Property  
 ; STREET: P.O. Box 1539 / UW2220  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/483,636  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/117366  
 ; FILING DATE: 07-SEP-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/136783  
 ; FILING DATE: 14-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US/94/10308  
 ; FILING DATE: 07-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sutton, Jeffrey A.  
 ; REGISTRATION NUMBER: 34,028  
 ; REFERENCE/DOCKET NUMBER: P50186-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 270-5024  
 ; TELEFAX: (215) 270-5090  
 ; INFORMATION FOR SEQ ID NO: 28:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-483-636-28

Query Match 83.3%; Score 40; DB 2; Length 9;  
 Best Local Similarity 87.5%; Pred. No. 2e+05;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



QY 1 QQSSEDP 8  
|11:1111  
Db 1 QQSNEP 8

## RESULT 14

US-08-483-632-28  
; Sequence 28, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA: PCT/US/94/10308  
; APPLICATION NUMBER: 34,028  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-632-28

Query Match 83.3%; Score 40; DB 2; Length 9;  
Best Local Similarity 87.5%; Pred. No. 2e+05; Indels 0;  
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QQSSEDP 8  
|11:1111  
Db 1 QQSNEP 8

## RESULT 15

US-08-483-636-14  
; Sequence 14, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.

; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA: PCT/US/94/10308  
; APPLICATION NUMBER: 34,028  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-636-14

Query Match 83.3%; Score 40; DB 2; Length 131;  
Best Local Similarity 87.5%; Pred. No. 4.2; Indels 0;  
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QQSSEDP 8  
|11:1111  
Db 112 QQSNEP 119

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Job time: 8.12903 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:15:53 : Search time 5.22581 Seconds  
(without alignments)  
44.001 Million cell updates/sec

Title: US-09-701-001B-6  
Perfect score: 48  
Sequence: 1 QQSSEDPPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description        |
|------------|-------|---------------|--------|-------|--------------------|
| 1          | 45    | 93.8          | 9      | 9     | US-09-879-461-20   |
| 2          | 45    | 93.8          | 112    | 9     | US-09-144-886-80   |
| 3          | 45    | 93.8          | 131    | 9     | US-09-879-461-58   |
| 4          | 45    | 93.8          | 132    | 9     | US-09-879-461-2    |
| 5          | 40    | 83.3          | 9      | 9     | US-09-879-461-28   |
| 6          | 40    | 83.3          | 131    | 9     | US-09-879-461-14   |
| 7          | 36    | 75.0          | 134    | 10    | US-09-881-823-2    |
| 8          | 36    | 75.0          | 412    | 9     | US-10-078-650-17   |
| 9          | 36    | 75.0          | 412    | 9     | US-10-094-649-2    |
| 10         | 35    | 72.9          | 112    | 9     | US-09-144-886-81   |
| 11         | 35    | 72.9          | 112    | 10    | US-09-810-502-36   |
| 12         | 35    | 72.9          | 112    | 10    | US-09-810-502-37   |
| 13         | 35    | 72.9          | 780    | 10    | US-09-771-161A-144 |
| 14         | 35    | 72.9          | 942    | 10    | US-09-771-161A-235 |
| 15         | 35    | 72.9          | 942    | 10    | US-09-771-161A-236 |
| 16         | 34    | 70.8          | 106    | 10    | US-09-802-077-6    |
| 17         | 34    | 70.8          | 106    | 10    | US-09-802-096-6    |
| 18         | 34    | 70.8          | 112    | 9     | US-09-144-886-87   |
| 19         | 34    | 70.8          | 218    | 10    | US-09-917-410-2    |

|    |      |     |    |                    |                     |
|----|------|-----|----|--------------------|---------------------|
| 20 | 68.8 | 61  | 9  | US-09-796-692-1514 | Sequence 1514, Appl |
| 21 | 68.8 | 97  | 9  | US-10-001-883-91   | Sequence 91, Appl   |
| 22 | 68.8 | 111 | 10 | US-09-802-077-2    | Sequence 2, Appl    |
| 23 | 68.8 | 111 | 10 | US-09-802-096-2    | Sequence 2, Appl    |
| 24 | 68.8 | 111 | 10 | US-09-920-171-5    | Sequence 5, Appl    |
| 25 | 68.8 | 111 | 10 | US-09-920-171-6    | Sequence 6, Appl    |
| 26 | 68.8 | 114 | 10 | US-09-920-171-8    | Sequence 8, Appl    |
| 27 | 68.8 | 114 | 10 | US-09-920-171-9    | Sequence 9, Appl    |
| 28 | 68.8 | 114 | 10 | US-09-920-171-10   | Sequence 10, Appl   |
| 29 | 68.8 | 175 | 10 | US-09-925-122A-3   | Sequence 3, Appl    |
| 30 | 68.8 | 218 | 10 | US-09-802-077-9    | Sequence 9, Appl    |
| 31 | 68.8 | 218 | 10 | US-09-802-096-9    | Sequence 9, Appl    |
| 32 | 68.8 | 218 | 10 | US-09-920-171-13   | Sequence 13, Appl   |
| 33 | 68.8 | 218 | 10 | US-09-920-171-15   | Sequence 15, Appl   |
| 34 | 68.8 | 218 | 10 | US-09-920-171-17   | Sequence 17, Appl   |
| 35 | 68.8 | 218 | 10 | US-09-920-171-19   | Sequence 19, Appl   |
| 36 | 68.8 | 218 | 10 | US-09-920-171-24   | Sequence 24, Appl   |
| 37 | 68.8 | 248 | 10 | US-09-920-171-22   | Sequence 22, Appl   |
| 38 | 68.8 | 248 | 10 | US-09-920-171-23   | Sequence 23, Appl   |
| 39 | 68.8 | 348 | 9  | US-09-738-626-4325 | Sequence 4325, Appl |
| 40 | 68.8 | 359 | 9  | US-09-712-363-269  | Sequence 269, Appl  |
| 41 | 66.7 | 92  | 10 | US-09-893-737-204  | Sequence 204, Appl  |
| 42 | 66.7 | 112 | 9  | US-09-144-886-84   | Sequence 84, Appl   |
| 43 | 66.7 | 112 | 9  | US-09-144-886-85   | Sequence 85, Appl   |
| 44 | 66.7 | 112 | 9  | US-09-144-886-86   | Sequence 86, Appl   |
| 45 | 66.7 | 112 | 9  | US-09-144-886-94   | Sequence 94, Appl   |

## ALIGNMENTS

RESULT 1  
US-09-879-461-20  
; Sequence 20, Application US/09879461  
; Publication No. US20020193575A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; Gross, Mitchell S.  
; Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: Corporate Intellectual Property, UW2220 - 709  
; Swedeland Rd.  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/879,461  
; FILING DATE: 12-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/612,929  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/136,783  
; FILING DATE: 14-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-879-461-20

Query Match          93.8%; Score 45; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
   |||:|||||
Db 1 QOSNEPDPT 9

RESULT 2
US-09-144-886-80
; Sequence 80, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 80
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bont/A clone
; OTHER INFORMATION: IB6 region VL epitope 1
US-09-144-886-80

Query Match          93.8%; Score 45; DB 9; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.28;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
   |||:|||||
Db 93 QOSNEPDPT 101

RESULT 3
US-09-879-461-58
; Sequence 58, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090

```

```

;
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-879-461-58

Query Match          93.8%; Score 45; DB 9; Length 131;
Best Local Similarity 88.9%; Pred. No. 0.33;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
   |||:|||||
Db 112 QOSNEPDPT 120

RESULT 4
US-09-879-461-2
; Sequence 2, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090

```

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-879-461-2

Query Match 93.8%; Score 45; DB 9; Length 132;  
Best Local Similarity 88.9%; Pred. No. 0.33;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
| | | : | | | | |  
DB 113 QQSNEPPT 121

LT 5

US-879-461-28  
Sequence 28, Application US/09879461  
Publication No. US20020193575A1  
GENERAL INFORMATION:  
APPLICANT: Holmes, Stephen D.  
Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation  
STREET: Corporate Intellectual Property, UW2220 - 709  
Swedeland Rd.  
CITY: King of Prussia  
STATE: PA

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,461

FILING DATE: 12-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/612,929

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/136,783

FILING DATE: 14-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-879-461-28

Query Match 83.3%; Score 40; DB 9; Length 9;

Best Local Similarity 87.5%; Pred. No. 1.2e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 8

| | | : | | | | |

DB 1 QQSNEPPT 8

RESULT 6

US-09-879-461-14

Sequence 14, Application US/09879461

Publication No. US20020193575A1

GENERAL INFORMATION:

APPLICANT: Holmes, Stephen D.

Gross, Mitchell S.

Sylvester, Daniel R.

TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in

Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: Corporate Intellectual Property, UW2220 - 709

Swedeland Rd.

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,461

FILING DATE: 12-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/612,929

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/136,783

FILING DATE: 14-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50186-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-879-461-14

Query Match 83.3%; Score 40; DB 9; Length 131;

Best Local Similarity 87.5%; Pred. No. 2.4;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 8

| | | : | | | | |

DB 112 QQSNEPPT 119

RESULT 7

US-09-881-823-2

Sequence 2, Application US/09881823

Patent No. US20020068066A1

GENERAL INFORMATION:

APPLICANT: SHI, WENYUAN

ANDERSON, MAXWELL

APPLICANT: MORRISON, SHERIE

APPLICANT: TRINH, RYAN

APPLICANT: WIMS, LETITIA

APPLICANT: CHEN, LI

TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries

```
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Murine
; ORGANISM: Murine
US-09-881-823-2
```

```
Query Match 75.0%; Score 36; DB 10; Length 134;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 QOSSEDPPT 9
Db 113 QONNADPPT 121
```

```
US-10-078-650-17
; Sequence 17, Application US/10078650
; Patent No. US20020169301A1
; GENERAL INFORMATION:
; APPLICANT: Fujimoto, Katsumi
; APPLICANT: Shin, Mei
; APPLICANT: Kato, Yukio
; TITLE OF INVENTION: NOVEL bHLH TYPE TRANSCRIPTION FACTOR
; FILE REFERENCE: 06501-101001
; CURRENT APPLICATION NUMBER: US/10/078,650
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/JP00/03991
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: JP 11-233286
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-078-650-17
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Query Match 75.0%; Score 36; DB 9; Length 412;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 QOSSEDPPT 9
Db 279 KOESEEPPT 287
```

```
US-10-094-649-2
; Sequence 2, Application US/10094649
; Publication No. US20030009020A1
; GENERAL INFORMATION:
; APPLICANT: Kawamoto, Takeshi
; APPLICANT: Kato, Yukio
; TITLE OF INVENTION: Gene Originating in Human Chondrocyte
; FILE REFERENCE: 46124-5014-US
; CURRENT APPLICATION NUMBER: US/10/094,649
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US/09/462,624
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 202227/1997
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: PCT/JP98/03106
; PRIOR FILING DATE: 1998-07-10
```

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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-649-2
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```
Query Match 75.0%; Score 36; DB 9; Length 412;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 QOSSEDPPT 9
Db 279 KOESEEPPT 287
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```
US-09-144-886-81
; Sequence 81, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500-117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1C9 region VL epitope 1
US-09-144-886-81
```

```
Query Match 72.9%; Score 35; DB 9; Length 112;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
Qy 1 QOSSEDPPT 9
Db 93 QOSNEDPPT 101
```

```
US-09-810-502-36
; Sequence 36, Application US/09810502
; Patent No. US20020034765A1
; GENERAL INFORMATION:
; APPLICANT: Padian, Eduardo A.
; APPLICANT: Daugherty, Bruce L.
; APPLICANT: Mark, George E.
```

```
; TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY
; OF ANTIBODY VARIABLE DOMAINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/810,502  
; FILING DATE: 16-Mar-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/905,280  
; FILING DATE: 01-Aug-1997  
; APPLICATION NUMBER: 08/609,218  
; FILING DATE: 01-Mar-1996  
; APPLICATION NUMBER: 08/109,187  
; FILING DATE: 19-Aug-1993  
; APPLICATION NUMBER: 07/702,217  
; FILING DATE: 17-May-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 184100C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-3905  
; TELEFAX: 732-594-4720  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-810-502-36

Query Match 72.9%; Score 35; DB 10; Length 112;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
Db 93 QQSNEDEPLT 101

## RESULT 12

US-09-810-502-37  
; Sequence 37, Application US/09810502  
; Patent No. US20020034765A1  
; GENERAL INFORMATION:  
; APPLICANT: Padlan, Eduardo A.  
; Daugherty, Bruce L.  
; Mark, George E.

TITLE OF INVENTION: A METHOD FOR REDUCING THE IMMUNOGENICITY  
OF ANTIBODY VARIABLE DOMAINS

NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/810,502  
FILING DATE: 16-Mar-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/905,280  
FILING DATE: 01-Aug-1997  
APPLICATION NUMBER: 08/609,218  
FILING DATE: 01-Mar-1996  
APPLICATION NUMBER: 08/109,187  
FILING DATE: 19-Aug-1993

; APPLICATION NUMBER: 07/702,217  
; FILING DATE: 17-May-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 184100C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-3905  
; TELEFAX: 732-594-4720  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-810-502-37

Query Match 72.9%; Score 35; DB 10; Length 112;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
Db 93 QQSNEDEPLT 101

## RESULT 13

US-09-771-161A-144  
; Sequence 144, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:

APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 144  
LENGTH: 780  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-771-161A-144

Query Match 72.9%; Score 35; DB 10; Length 780;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
Db 564 QKSRRDPPS 572

## RESULT 14

US-09-771-161A-235  
; Sequence 235, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:

APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 235  
; LENGTH: 942  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-235

Query Match 72.9%; Score 35; DB 10; Length 942;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
DB 564 QKSRDPPS 572

BLT 15  
US-09-771-161A-236  
; Sequence 236, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 236  
; LENGTH: 942  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-236

Query Match 72.9%; Score 35; DB 10; Length 942;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
DB 564 QKSRDPPS 572

Search completed: February 14, 2003, 11:21:32  
Job time : 6.22581 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:12:02 ; Search time 9 Seconds  
(without alignments)  
96.134 Million cell updates/sec

Title: US-09-701-001b-6  
Perfect score: 48  
Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73: \*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 48    | 100.0       | 112    | 2 S19971 | Ig kappa chain V r |
| 2          | 48    | 100.0       | 131    | 2 PH1226 | Ig kappa chain pre |
| 3          | 38    | 79.2        | 112    | 2 S19972 | Ig kappa chain V r |
| 4          | 38    | 79.2        | 301    | 2 T45859 | R2R3-MVB transcrip |
| 5          | 38    | 79.2        | 304    | 1 S71285 | myb-related protei |
| 6          | 37    | 77.1        | 508    | 2 F84921 | hypothetical prote |
| 7          | 36    | 75.0        | 65     | 2 C38601 | Ig kappa chain V r |
| 8          | 35    | 75.0        | 412    | 2 JC5547 | basic helix-loop-h |
| 9          | 35    | 72.9        | 96     | 2 B49442 | Ig light chain V r |
| 10         | 35    | 72.9        | 102    | 2 PH1079 | Ig light chain V r |
| 11         | 35    | 72.9        | 107    | 2 S26344 | Ig kappa chain V r |
| 12         | 35    | 72.9        | 111    | 1 KVMS37 | Ig kappa chain V r |
| 13         | 35    | 72.9        | 111    | 1 KVMS37 | Ig kappa chain V r |
| 14         | 35    | 72.9        | 111    | 1 KVMS83 | Ig kappa chain V r |
| 15         | 35    | 72.9        | 111    | 2 S09866 | Ig kappa chain V-J |
| 16         | 35    | 72.9        | 111    | 2 A33936 | Ig kappa chain V r |
| 17         | 35    | 72.9        | 479    | 2 S48705 | serine/threonine p |
| 18         | 35    | 72.9        | 942    | 2 JC2129 | protein kinase PKN |
| 19         | 35    | 72.9        | 950    | 2 S27473 | URB51 protein - sm |
| 20         | 34    | 70.8        | 107    | 2 S26343 | Ig kappa chain V r |
| 21         | 34    | 70.8        | 111    | 1 KVMS43 | Ig kappa chain V r |
| 22         | 34    | 70.8        | 111    | 1 KVMS08 | Ig kappa chain V r |
| 23         | 34    | 70.8        | 111    | 1 KVMS69 | Ig kappa chain V r |
| 24         | 34    | 70.8        | 127    | 2 B4172  | hypothetical prote |
| 25         | 34    | 70.8        | 268    | 2 T51678 | myb-related transc |
| 26         | 34    | 70.8        | 320    | 2 C85440 | myb-related protei |
| 27         | 34    | 70.8        | 355    | 2 AB0034 | probable type III  |
| 28         | 34    | 70.8        | 794    | 2 T27870 | hypothetical prote |
| 29         | 34    | 70.8        | 925    | 2 JC2033 | G protein-coupled  |

|    |    |      |      |          |                    |
|----|----|------|------|----------|--------------------|
| 30 | 34 | 70.8 | 1006 | 2 T00050 | hypothetical prote |
| 31 | 34 | 70.8 | 1027 | 2 I38604 | p53-binding protei |
| 32 | 34 | 70.8 | 3149 | 1 QJBEB  | BPLF1 protein - hu |
| 33 | 33 | 68.8 | 62   | 1 NINJIM | short neurotoxin 1 |
| 34 | 33 | 68.8 | 81   | 2 S42193 | Ig kappa chain V r |
| 35 | 33 | 68.8 | 87   | 2 C97796 | hypothetical prote |
| 36 | 33 | 68.8 | 111  | 2 D45722 | anti-glycoprotein  |
| 37 | 33 | 68.8 | 135  | 2 D82539 | hypothetical prote |
| 38 | 33 | 68.8 | 192  | 2 T35200 | hypothetical prote |
| 39 | 33 | 68.8 | 359  | 2 A70978 | probable rmlA2 pro |
| 40 | 33 | 68.8 | 491  | 2 JE0276 | voltage-gated pota |
| 41 | 33 | 68.8 | 731  | 2 S46813 | lanosterol synthas |
| 42 | 33 | 68.8 | 786  | 2 A55501 | cyclin F - human   |
| 43 | 33 | 68.8 | 1094 | 2 S49313 | protein kinase - s |
| 44 | 33 | 68.8 | 1392 | 2 A43336 | microtubule-vesicl |
| 45 | 33 | 68.8 | 1427 | 2 S22695 | restin - human     |

## ALIGNMENTS

### RESULT 1

S19971

Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
R:Accession: S19971; S19973  
R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: S19963  
A:Accession: S19971  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289  
A:Experimental source: clone M-T310  
A:Accession: S19973  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEW>  
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293  
A:Experimental source: M-T404  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
Db 93 QOSSEDPPT 101

### RESULT 2

PH1226

Ig kappa chain precursor V region (M-T310) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000

R:Accession: PH1226

R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; L

Gene 121, 271-278, 1992

A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and

A:Reference number: PH1224; MUID:93077041; PMID:1446824

A:Accession: PH1226

A:Molecule type: mRNA

A:Residues: 1-131 <WEI>

A:Cross-references: GB:S50265; NID:g260765; PIDN:AA24320.1; PID:g260766

A>Note: this mouse sequence was hybridized and fused with a human constant region gen

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-131/Product: Ig light chain V region #status predicted <MAT>

F;36-114/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 48; DB 2; Length 131;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9  
|||||

Db 113 QOSSEDPPT 121

RESULT 3

S19972

Ig kappa chain V region (M-T321) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S19972

R:Weissenhorn, W.; Riethmuller, G.; Weiss, E.M.; Rieber, E.P.

submitted to the EMBL Data Library, March 1992

A:Description: Structural characterization of CD4 mAb.

A:Reference number: S19963

C:Accession: S19972

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <WEI>

A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 38; DB 2; Length 112;

Best Local Similarity 88.9%; Pred. No. 4.2;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9

|||||

Db 93 QOSSEDPPT 101

RESULT 4

T45859

R2R3-MYB transcription factor - Arabidopsis thaliana

N:Alternate names: protein F3A4.140

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Mar-2000

C:Accession: T45859

R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23007

C:Accession: T45859

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 <BAR>

A:Cross-references: EMBL:AL132978

A:Experimental source: cultivar Columbia; BAC clone F3A4

C:Genetics:

A:Map position: 3

A:Note: F3A4.140

C:Superfamily: Arabidopsis myb-related 33.2K protein; myb DNA-binding repeat homology

Query Match 79.2%; Score 38; DB 2; Length 301;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9

|||||

Db 197 SSEDPT 203

RESULT 5

S71285

myb-related protein, 33.2K - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 16-Jun-2000

C:Accession: S71285

R:Kirik, V.; Baumlein, H.

submitted to the EMBL Data Library, September 1995

A:Description: Characterization of two cDNAs encoding MYB-related proteins in Arabid

A:Reference number: S71285

A:Accession: S71285

A:Molecule type: mRNA

A:Residues: 1-304 <KIR>

A:Cross-references: EMBL:Z54137; NID:g1263096; PIDN:CAA90810.1; PID:g1263097

C:Superfamily: Arabidopsis myb-related 33.2K protein; myb DNA-binding repeat homology

C:Keywords: DNA binding; duplication

F;1-52/Domain: myb DNA-binding repeat homology <MYB1>

F;53-103/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 79.2%; Score 38; DB 1; Length 304;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9

|||||

Db 197 SSEDPT 203

RESULT 6

F84921

Hypothetical protein At2g47960 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: F84921

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84921

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-508 <STO>

A:Cross-references: GB:AE002093; NID:g3738308; PIDN:AAC63650.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g47960

A:Map position: 2

Query Match 77.1%; Score 37; DB 2; Length 508;

Best Local Similarity 66.7%; Pred. No. 33;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSSEDPPT 9

|||||

Db 241 EDSTEDPT 249

RESULT 7

C38601

Ig kappa chain V region (2B5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999

C:Accession: C38601

R:Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A:Title: Common structural features among monoclonal antibodies binding the same anti

A:Reference number: A38601; MUID:91115823; PMID:1703527

A:Accession: C38601

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-65 <GOS>

A:Cross-references: GB:M57980; NID:g196406; PIDN:AAA63361.1; PID:g196407

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match

75.0%; Score 36; DB 2; Length 65;

Best Local Similarity 77.8%; Pred. No. 5.5;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
|||:|||||  
Db 46 QQSNEPPT 54

## RESULT 8

JC5547  
basic helix-loop-helix factor DEC1 - human  
C:Species: Homo sapiens (man)  
C>Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 21-Jul-2000  
C:Accession: JC5547  
R;Shen, M.; Kawamoto, T.; Yan, W.; Nakamasu, K.; Tamagami, M.; Koyano, Y.; Noshiro, M.;  
Biochem. Biophys. Res. Commun. 236, 294-298, 1997  
A:Title: Molecular characterization of the novel basic helix-loop-helix protein DEC1 ex  
Reference number: JC5547; MUID:97382424; PMID:9240428  
Molecule type: mRNA  
Accession: JC5547  
A:Residues: 1-412 <SHE>  
A:Cross-references: DBJ:AB004066; NID:q2308996; PIDN:BAA21720.1; PID:q2308997  
C:Comment: This protein is involved in the control of cell differentiation in several ti  
F:51-108/Region: helix-loop-helix #status predicted

Query Match 75.0%; Score 36; DB 2; Length 412;  
Best Local Similarity 66.7%; Pred. No. 40;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
:|||||  
Db 279 QQSSEPT 287

## RESULT 9

B49442  
Ig light chain V region (50.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: B49442  
R;Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; S  
Proteins 14, 499-508, 1992  
A:Title: Crystallization, sequence, and preliminary crystallographic data for an antipep  
A:Reference number: A49442; MUID:93066166; PMID:1438187  
A:Accession: B49442  
A:Status: preliminary; not compared with conceptual translation  
Molecule type: DNA  
Residues: 1-96 <STU>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:8-86/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 96;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
|||:|||||  
Db 85 QQSNEPPT 93

## RESULT 10

PH1079  
Ig light chain V region (clone 202.38m) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1079  
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c  
A:Reference number: PH0971; MUID:92381444; PMID:1512540  
A:Accession: PH1079  
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA  
A:Residues: 1-102 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 102;  
Best Local Similarity 77.8%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
|||:|||||  
Db 93 QQSKEVPPT 101

## RESULT 11

S26344  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26344  
R;Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protei  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26344  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <STA>  
A:Cross-references: EMBL:X59209; NID:q52336; PIDN:CAA41919.1; PID:g1334074  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 107;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
|||:|||||  
Db 92 QQSNEPPT 100

## RESULT 12

KVMS37  
Ig kappa chain V regions (PC3741, T111) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 21-Jan-2000  
C:Accession: A93204; A93822; A01934  
R;Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152; PMID:103003  
A:Contents: PC3741  
A:Accession: A93204  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
R;McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related  
A:Reference number: A93822; MUID:79012520; PMID:99744  
A:Contents: T111  
A:Accession: A93822  
A:Molecule type: protein  
A:Residues: 1-111 <MCK>  
C:Complex: An immunoglobulin heterotetramer consists of two identical light (C  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 72.9%; Score 35; DB 1; Length 111;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QOSSEDPPT 9  
| | | : | | | |  
Db 93 QOSNEDPYT 101

RESULT 13  
KWMS01  
Ig kappa chain V region (CBPC 101) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000  
C:Accession: A01936  
R:McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related molecules  
A:Reference number: A93822; MUID:79012520; PMID:99744  
A:Accession: A01936  
A:Molecule type: protein  
A:Residues: 1-111 <MCK>  
Comment: This chain was isolated from a myeloma protein.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 72.9%; Score 35; DB 1; Length 111;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QOSSEDPPT 9  
| | | : | | | |  
Db 93 QOSNEDPYT 101

RESULT 14  
KWMS83  
Ig kappa chain V region (PC7183) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: B01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152; PMID:103003  
A:Accession: B01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 72.9%; Score 35; DB 1; Length 111;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QOSSEDPPT 9  
| | | : | | | |  
Db 93 QOSNEDPYT 101

RESULT 15  
S09966  
Ig kappa chain V-J region (1E10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 21-Jan-2000

C:Accession: S09966  
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.  
Eur. J. Immunol. 20, 771-777, 1990  
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies  
A:Reference number: S09955; MUID:90269328; PMID:2347362  
A:Accession: S09966  
A:Molecule type: mRNA  
A:Residues: 1-111 <REI>  
A:Cross-references: EMBL:X51854; NID:955397; PIDN:CAA36147.1; PID:9930231  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 111;  
Best Local Similarity 77.8%; Pred. No. 15;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QOSSEDPPT 9  
| | | : | | | |  
Db 93 QOSNEDPYT 101

Search completed: February 14, 2003, 11:19:48  
Job time : 10 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:05:27 ; Search time 4.64516 Seconds  
(without alignments)  
80.360 Million cell updates/sec

Title: US-09-701-001B-6  
Perfect score: 48  
Sequence: 1 QSSSEDPPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 36    | 75.0        | 411    | 1 BHB2_MOUSE | O35185 mus musculus |
| 2          | 36    | 75.0        | 411    | 1 BHB2_RAT   | O35780 rattus norv  |
| 3          | 36    | 75.0        | 412    | 1 BHB2_HUMAN | O45033 homo sapien  |
| 4          | 35    | 72.9        | 111    | 1 KV3H_MOUSE | P01660 mus musculus |
| 5          | 35    | 72.9        | 111    | 1 KV3L_MOUSE | P01664 mus musculus |
| 6          | 35    | 72.9        | 111    | 1 KV3N_MOUSE | P01666 mus musculus |
| 7          | 35    | 72.9        | 942    | 1 PKL1_HUMAN | O16512 homo sapien  |
| 8          | 35    | 72.9        | 950    | 1 UBL1_MOUSE | P40349 ustilago ma  |
| 9          | 34    | 70.8        | 111    | 1 KV3M_MOUSE | P01665 mus musculus |
| 10         | 34    | 70.8        | 111    | 1 KV3O_MOUSE | P01667 mus musculus |
| 11         | 34    | 70.8        | 111    | 1 KV3Q_MOUSE | P01669 mus musculus |
| 12         | 34    | 70.8        | 215    | 1 VIF_HV2NZ  | P05901 human immun  |
| 13         | 34    | 70.8        | 232    | 1 SPIH_HUMAN | O99865 homo sapien  |
| 14         | 34    | 70.8        | 925    | 1 GLHR_ANTEL | P35409 anthopleura  |
| 15         | 34    | 70.8        | 1972   | 1 P53L_HUMAN | Q28888 homo sapien  |
| 16         | 34    | 70.8        | 3149   | 1 TEGU_EBV   | P01431 naja mossam  |
| 17         | 33    | 68.8        | 62     | 1 NXSL_NAJMO | O70624 human immun  |
| 18         | 33    | 68.8        | 118    | 1 REV_HV1LW  | O88396 mus musculus |
| 19         | 33    | 68.8        | 224    | 1 GRE2_MOUSE | Q15642 homo sapien  |
| 20         | 33    | 68.8        | 545    | 1 CIP4_HUMAN | P38604 saccharomyc  |
| 21         | 33    | 68.8        | 730    | 1 ERG7_YEAST | P41002 homo sapien  |
| 22         | 33    | 68.8        | 786    | 1 CG2F_HUMAN | O88879 mus musculus |
| 23         | 33    | 68.8        | 1249   | 1 APAF_MOUSE | Q9epv5 rattus norv  |
| 24         | 33    | 68.8        | 1249   | 1 APAF_RAT   | P30622 homo sapien  |
| 25         | 33    | 68.8        | 1427   | 1 REST_HUMAN | P01662 mus musculus |
| 26         | 32    | 66.7        | 111    | 1 KV3J_MOUSE | P01663 mus musculus |
| 27         | 32    | 66.7        | 111    | 1 KV3K_MOUSE | P09711 human cytom  |
| 28         | 32    | 66.7        | 277    | 1 J1L1_HCMVA | O93379 ictalurine p |
| 29         | 32    | 66.7        | 376    | 1 P53_ICTPU  | P97497 mus musculus |
| 30         | 32    | 66.7        | 403    | 1 SHBG_MOUSE | P54998 rhodococcus  |
| 31         | 32    | 66.7        | 417    | 1 SOXC_RHOSO | Q01988 canis famil  |
| 32         | 32    | 66.7        | 445    | 1 UBPE_CANFA | O00515 homo sapien  |
| 33         | 32    | 66.7        | 517    | 1 LAD1_HUMAN |                     |

## ALIGNMENTS

### RESULT 1

| ID | BHB2_MOUSE   | STANDARD; | PRT; | 411 AA. |
|----|--|-----------|------|---------|
| AC | O35185; P97289;  |           |      |         |
| DT | 15-JUN-2002 (Rel. 41, Created)   |           |      |         |
| DT | 15-JUN-2002 (Rel. 41, Last sequence update)  |           |      |         |
| DE | Class B basic helix-loop-helix protein 2 (BHLHB2) (Stimulated with retinoic acid 13) (E47 interaction protein 1) (eip1).   |           |      |         |
| GN | BHLHB2 OR STRA13 OR CLAST5.  |           |      |         |
| OS | Mus musculus (Mouse).  |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |           |      |         |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |           |      |         |
| OX | NCBI_TaxID=10090;  |           |      |         |
| RN | [1]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RC | TISSUE=Embryonic carcinoma;  |           |      |         |
| RX | MEDLINE=97427857; PubMed=9284045;  |           |      |         |
| RA | Boudjelal M., Taneja R., Matsubara S., Bouillet P., Dolle P., Chambon P.;  |           |      |         |
| RT | "Overexpression of Stral3, a novel retinoic acid-inducible gene of the basic helix-loop-helix family, inhibits mesodermal and promotes neuronal differentiation of Pl9 cells.";  |           |      |         |
| RT | Genes Dev. 11:2052-2065(1997).   |           |      |         |
| RL | [2]  |           |      |         |
| RN | SEQUENCE FROM N.A., AND INTERACTION WITH E47/TCF3.   |           |      |         |
| RP | STRAIN=BALB/c;   |           |      |         |
| RC | MEDLINE=97203270; PubMed=9050988;  |           |      |         |
| RX | Dear T.N., Hainzl T., Follo M., Wilmore H., Matena K., Boehm T.;   |           |      |         |
| RA | "Identification of interaction partners for the basic-helix-loop-helix protein E47.";  |           |      |         |
| RT | Oncogene 14:891-898(1997).   |           |      |         |
| RL | [3]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RC | STRAIN=C57BL/6; TISSUE=Spleen;   |           |      |         |
| RA | O-Wang J.;   |           |      |         |
| RT | Isolation of a CD40-activated gene from murine splenic B cells.";  |           |      |         |
| RL | Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  |           |      |         |
| RN | [4]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RC | TISSUE=Mammary gland;  |           |      |         |
| RA | Straussberg R.;  |           |      |         |
| RL | Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  |           |      |         |
| CC | -!- FUNCTION: May function as a transcriptional factor for neuronal differentiation.   |           |      |         |
| CC | -!- SUBUNIT: Able to homodimerize or heterodimerize with E47.  |           |      |         |
| CC | -!- SUBCELLULAR LOCATION: Nuclear (By similarity).   |           |      |         |
| CC | -!- DEVELOPMENTAL STAGE: Expressed from E9.5 day to E17.5 day in the ventricular layer of the brain and spinal cord, but also in the retinal pigment epithelium, developing eyelids, nasal epithelium, serous gland, vibrissae, epithelium of the mouth cavity and the tooth buds. Highly expressed in the heart, thymus and adrenal glands followed by lung, liver parenchyma, kidney tubules, epithelium of the esophagus and stomach. From E15.5 to E17.5 it is expressed in urinary bladder and urethra. From E17.5, it is |           |      |         |

O9umx9 homo sapien  
P45897 caenorhabdi  
P20794 homo sapien  
Q61545 mus musculu  
Q01844 homo sapien  
P24482 saccharomyc  
Q60446 cricetus  
Q92598 homo sapien  
Q61699 mus musculu  
P52593 saccharomyc  
P07293 oryctolagus  
P05830 escherichia

34 32 66.7 530 1 MATP\_HUMAN  
35 32 66.7 570 1 SMA4\_CAEEL  
36 32 66.7 623 1 MAK\_HUMAN  
37 32 66.7 655 1 EWS\_MOUSE  
38 32 66.7 656 1 EWS\_HUMAN  
39 32 66.7 692 1 DPB2\_YEAST  
40 32 66.7 858 1 H105\_CRIGR  
41 32 66.7 858 1 H105\_HUMAN  
42 32 66.7 858 1 H105\_MOUSE  
43 32 66.7 1655 1 NI88\_YEAST  
44 32 66.7 1873 1 CCAS\_RABIT  
45 31 64.6 93 1 REPI\_ECOLI

CC expressed in developing muscle.  
CC -!- INDUCTION: Stimulated by retinoic acid (RA).  
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS.  
CC -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AF010305; AAB64228.1; -.  
CC EMBL: Y07836; CAAG9169.1; -.  
CC EMBL: AF364051; AAK50859.1; -.  
CC EMBL: BC010720; AAH10720.1; -.  
CC MGD; MGI:1097714; Bhlhb2.  
CC InterPro: IPR001092; HLH\_basic.  
CC InterPro: IPR003650; Orange.  
CC Pfam: PF00010; HLH; 1.  
CC SMART; SM00353; HLH; 1.  
CC SMART; SM00511; ORANGE; 1.  
CC PROSITE; PS00038; HLH\_1; 1.  
CC PROSITE; PS00888; HLH\_2; 1.  
CC Transcription regulation; DNA-binding; Nuclear protein.  
CC DNA\_BIND 53 65 BASIC DOMAIN.  
CC DOMAIN 66 108 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
CC DOMAIN 140 184 ORANGE.  
CC CONFLICT 288 288 K -> T (IN REF. 2).  
CC SEQUENCE 411 AA; 45360 MW; B392893CD49292BC CRC64;  
SQ

Query Match 75.0%; Score 36; DB 1; Length 411;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
Db 279 KOSEEPPT 287

RESULT 2  
BHB2\_RAT  
ID BHB2\_RAT STANDARD; PRT; 411 AA.  
AC O35780.  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Class B basic helix-loop-helix protein 2 (bHLHB2) (Enhancer-of-split  
DE and hairy-related protein 2) (SHARP-2).  
GN BHLHB2 OR SHARP2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Sprague-Dawley; TISSUE=Hippocampus;  
RX MEDLINE=98193761; PubMed=9532582;  
RA Rossner M.J., Doerr J., Gass P., Schwab M.H., Nave K.-A.;  
RT "SHARPs: mammalian enhancer-of-split- and hairy-related proteins  
RT coupled to neuronal stimulation.";  
RL Mol. Cell. Neurosci. 10:460-475(1997).  
CC -!- FUNCTION: May function as a transcriptional factor for neuronal  
CC differentiation.  
CC -!- SUBUNIT: Able to homodimerize or heterodimerize with E47 (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,  
CC liver, muscle, kidney, uterus and gut.  
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS.

CC -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC

CC EMBL: AF009330; AAB63587.1; -.  
CC InterPro: IPR001092; HLH\_basic.  
CC InterPro: IPR003650; Orange.  
CC Pfam: PF00010; HLH; 1.  
CC SMART; SM00353; HLH; 1.  
CC SMART; SM00511; ORANGE; 1.  
CC PROSITE; PS00038; HLH\_1; 1.  
CC PROSITE; PS00888; HLH\_2; 1.  
CC Transcription regulation; DNA-binding; Nuclear protein.  
CC DNA\_BIND 53 65 BASIC DOMAIN.  
CC DOMAIN 66 108 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).  
CC DOMAIN 140 184 ORANGE.  
CC SEQUENCE 411 AA; 45529 MW; E56BD468D08824AD CRC64;  
SQ

Query Match 75.0%; Score 36; DB 1; Length 411;  
Best Local Similarity 66.7%; Pred. No. 14;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
Db 279 KOSEEPPT 287

RESULT 3  
BHB2\_HUMAN  
ID BHB2\_HUMAN STANDARD; PRT; 412 AA.  
AC O14503; Q96TD3;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Class B basic helix-loop-helix protein 2 (bHLHB2) (Differentially  
DE expressed in chondrocytes protein 1) (DEC1) (Enhancer-of-split and  
DE hairy-related protein 2) (SHARP-2) (Stimulated with retinoic acid 13).  
GN BHLHB2 OR DEC1 OR SHARP2 OR STRA13.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cartilage;  
RX MEDLINE=97382424; PubMed=9240428;  
RA Shen M., Kawamoto T., Yan W., Nakamasu K., Tamagami M., Koyano Y.,  
RA Noshiro M., Kato Y.;  
RT "Molecular characterization of the novel basic helix-loop-helix  
RT protein DEC1 expressed in differentiated human embryo chondrocytes.";  
RL Biochem. Biophys. Res. Commun. 236:294-298(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RX MEDLINE=21125593; PubMed=11226878;  
RA Teramoto M., Nakamasu K., Noshiro M., Matsuda Y., Gotoh O., Shen M.,  
RA Tsutsumi S., Kawamoto T., Iwamoto Y., Kato Y.;  
RT "Gene structure and chromosomal location of a human bHLH  
RT transcriptional factor DEC1 x Stra13 x SHARP-2/bHLHB2.";  
RL J. Biochem. 129:391-396(2001).  
RN [3]  
RP SEQUENCE OF 4-412 FROM N.A.  
RC  
RA Ivanov S.V., Lerman M.I.;  
RT "Exon-intron structure of the human STRA13(DEC1) bHLH transcription  
RT factor gene.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]

```
RP UBIOUITINATION.
RX MEDLINE=21226780; PubMed=11278694;
RA Ivanova A.V., Ivanov S.V., Danilkovitch-Miagkova A., Lerman M.I.;
RT "Regulation of STRA13 by the von Hippel-Lindau tumor suppressor
RT protein, hypoxia, and the UBC9/ubiquitin proteasome degradation
RT pathway.";
RL J. Biol. Chem. 276:15306-15315(2001).
CC -!- FUNCTION: May function as a transcriptional factor to modulate
CC chondrogenesis in response to the CAMP pathway.
CC -!- SUBUNIT: Able to homodimerize or heterodimerize with E47.
CC Interacts with ubiquitin-conjugating enzyme (UBC9).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Expressed in cartilage, spleen, intestine,
CC lung, and to a lesser extent in heart, brain, liver, muscle and
CC stomach.
CC -!- PTM: Association with UBC9 may target the protein for proteolysis
CC by the ubiquitin-dependent proteasome pathway.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSSCRIPTION FACTORS.
CC -!- SIMILARITY: CONTAINS 1 ORANGE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB004066; BAA21720.1; -
DR EMBL; AB043885; BAB18563.1; -
DR EMBL; AF353635; AAK49525.1; -
DR EMBL; AF353634; AAK49525.1; JOINED.
DR GenBank; HGNC:1046; BHLHB2.
DR MIM; 604256; -
DR InterPro; IPR001092; HLH_bas.
DR InterPro; IPR003650; Orange.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00511; ORANGE; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00888; HLH_2; 1.
DR Transcription regulation; DNA-binding; Nuclear protein;
KW Ub1 conjugation.
FT DNA_BIND 53 65
FT DOMAIN 66 108
FT DOMAIN 140 184
FT ORANGE
SEQUENCE 412 AA; 45510 MW; 2D73A3D4980793E5 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 412;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSESPPPT 9
DB 279 KOSEEPPT 287

RESULT 4
KV3H_MOUSE
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;

QY 1 QOSESPPPT 9
DB 279 KOSEEPPT 287
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RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM537.
DR HSSP; P01679; 2FB7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 54 60
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 93 101
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111
FT FRAMEWORK-4.
FT DISULFID 23 92
FT NON_TER 111 111
FT SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSESPPPT 9
DB 93 QQSNEPPT 101

RESULT 5
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 54 60
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 93 101
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111
FT FRAMEWORK-4.
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FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 93 QOSNEPDT 101

RESULT 6
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DB Ig kappa chain V-III region PC 7183.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KWS83.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 4.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
Db 93 QOSNEPDT 101

RESULT 7
ID PKL1_HUMAN STANDARD; PRT; 942 AA.
AC Q16512; Q15143;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C-like 1 (EC 2.7.1.-) (Protein-kinase C-related kinase
DE 1) (Protein kinase C-like PKN) (Serine-threonine protein kinase N).
GN PRKCL1 OR PRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95080426; PubMed=7988719;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
products.";
RL FEBS Lett. 356:5-8(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95154310; PubMed=7851406;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Cloning and expression patterns of two members of a novel protein-
kinase-C-related kinase family.";
RL Eur. J. Biochem. 227:344-351(1995).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-644.
RC TISSUE=Hippocampus;
RX MEDLINE=94183274; PubMed=8135837;
RA Mukai H., Ouo Y.;
RT "A novel protein kinase with leucine zipper-like sequences: its
catalytic domain is highly homologous to that of protein kinase C.";
RL Biochem. Biophys. Res. Commun. 199:897-904(1994).
CC -1- FUNCTION: CAN PHOSPHORYLATE RIBOSOMAL PROTEIN S6. MEDIATES GTPASE
RHO DEPENDENT INTRACELLULAR SIGNALING (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: FOUND UBQUITOUSLY. EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.
CC -1- PTM: AUTOPHOSPHORYLATED; PREFERABLY IN SERINE.
CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
-----
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-----
EMBL; U33053; AAC50209.1; -
EMBL; S75546; AAB33345.1; -
EMBL; D26181; BAA05169.1; -
DR HSP; P05132; IATP.
DR Genew; HGNC:9405; PRKCL1.
DR MIM; 601032; -
DR InterPro; IPR000008; C2.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000861; REM_repeat.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF02185; HR1_3.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00074; HR1_3.
DR SMART; SM00133; S-TK_X; 1.
DR SMART; SM00220; S-TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; ATP-binding; Serine/threonine-protein kinase;
phosphorylation.
FT DOMAIN 615 874 PROTEIN KINASE.
FT NP_BIND 621 629 ATP (BY SIMILARITY).
FT BINDING 644 644 ATP (BY SIMILARITY).
FT ACT_SITE 740 740 BY SIMILARITY.

```



FT MUTAGEN 644 644 K->R: SUBSTANTIAL REDUCTION OF  
FT CONFLICT 191 191 D -> G (IN REF. 3).  
SQ SEQUENCE 942 AA; 103989 MW; A89E40DCAEF560E3 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 942;  
Best Local Similarity 66.7%; Pred. No. 53;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

Db 564 QKSSRDPPS 572

RESULT 8

ID URB1\_USTMA STANDARD; PRT; 950 AA.  
AC P40349;  
01-FEB-1995 (Rel. 31, Created)  
01-FEB-1995 (Rel. 31, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
GN URB1.  
OS Ustilago maydis (Smut fungus).  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=5270;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=518;  
RX MEDLINE=94019380; PubMed=8413298;  
RA Volzard C.P., Wang J., McEvoy J.L., Xu P., Leong S.A.;  
RT "urbs1, a gene regulating siderophore biosynthesis in Ustilago  
RT maydis, encodes a protein similar to the erythroid transcription  
RT factor GATA-1.";  
RL Mol. Cell. Biol. 13:7091-7100(1993).

CC -!- FUNCTION: INVOLVED IN THE REGULATION OF SECRETED FERRIC IRON TYPE  
CC SIDEROPHORES. ACTS DIRECTLY OR INDIRECTLY TO REPRESS THE  
CC BIOSYNTHESIS OF SIDEROPHORES.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -!- SIMILARITY: CONTAINS 2 GATA-TYPE ZINC FINGERS.

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DR EMBL; M80547; AAB05617.1; -.

DR PIR; S27473; S27473.

DR HSP; P17679; LGNF.

DR TRANSFAC; T02406; -.

DR InterPro; IPR000679; Znf\_GATA.

DR InterPro; IPR001164; hRIP\_like.

DR Pfam; PF003320; GATA; 2.

DR PRINTS; PR00619; GATAZNFINGER.

DR SMART; SM00401; Znf\_GATA; 2.

DR PROSITE; PS00344; GATA\_ZN\_FINGER\_1; 2.

DR PROSITE; PS00114; GATA\_ZN\_FINGER\_2; 2.

KW DNA-binding; Zinc-finger; Transcription regulation; Repressor;

KW Nuclear protein.

FT ZN\_FING 338 362 GATA-TYPE 1.

FT ZN\_FING 482 506 GATA-TYPE 2.

FT DOMAIN 24 27 POLY-ALA.

FT DOMAIN 28 36 POLY-SER.

FT DOMAIN 487 490 POLY-THR.

FT DOMAIN 753 780 HIS-RICH.

FT DOMAIN 902 906 POLY-SER.

SQ SEQUENCE 950 AA; 101427 MW; F969C6DA09A78C12 CRC64;

Query Match

72.9%; Score 35; DB 1; Length 950;

Best Local Similarity 85.7%; Pred. No. 53;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOSSEDPPT 8

Db 448 QTSSEDPPT 454

RESULT 9

ID KV3M\_MOUSE STANDARD; PRT; 111 AA.  
AC P01665;  
21-JUL-1986 (Rel. 01, Created)  
21-JUL-1986 (Rel. 01, Last sequence update)  
15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 7043.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

RT diversity.";

RL Nature 276:785-790(1978).

DR PIR; A01937; KVMS43.

DR HSP; P80362; 1WTL.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR immunoglobulin V region.

KW DOMAIN 1 23

FT DOMAIN 24 38

FT DOMAIN 39 53

FT DOMAIN 54 60

FT DOMAIN 61 92

FT DOMAIN 93 101

FT DOMAIN 102 111

FT DISULFID 23 92

FT NON\_TER 111 111

SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 111;

Best Local Similarity 77.8%; Pred. No. 7.7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9

Db 93 QOSNEDPPT 101

RESULT 10

KV3O\_MOUSE

ID KV3O\_MOUSE STANDARD; PRT; 111 AA.

AC P01667;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region PC 6308.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gattaitan L., Loh E., Schilling J., Hood L.E.;

RT "Rearrangement of genetic information may produce immunoglobulin

RT diversity.";

RL Nature 276:785-790(1978).

Fri Feb 14 15:00:59 2003

us-09-701-001b-6.rsp

```
DR PIR; C01937; KVM508.
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 29 53
FT DOMAIN 39 60
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADB4D6C256D29 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 7.7;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

1 QOSSEDPPT 9
111:11111
Db 93 QOSNEDPWT 101

RESULT 11
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity".
RL Nature 276:785-790(1978).
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 29 53
FT DOMAIN 39 60
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 70.8%; Score 34; DB 1; Length 111;
Best Local Similarity 77.8%; Pred. No. 7.7;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

1 QOSSEDPPT 9
111:11111
Db 93 QOSNEDPWT 101

PIR; C01937; KVM508.
PRT; 215 AA.
ID VIF_HV2NZ STANDARD; PRT; 215 AA.
AC P05901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein) (Q protein).
GN VIF.
OS Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88320359; PubMed=3261862;
RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R.,
RA Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F.,
RA Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;
RT "Genetic variability between isolates of human immunodeficiency virus
RT (HIV) type 2 is comparable to the variability among HIV type 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC -----
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CC -----
CC EMBL; J03654; AAB00756.1; -
CC HIV; J03654; VIF52NHZ.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
CC AIDS.
KW AIDS.
SQ SEQUENCE 215 AA; 25321 MW; 9BAALF36A9690BFC CRC64;

Query Match 70.8%; Score 34; DB 1; Length 215;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9
1:11111
Db 192 QRGSESPPT 200

RESULT 13
SPIH_HUMAN STANDARD; PRT; 232 AA.
AC Q99865; O75650; Q9UJU0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Spindlin homolog (Protein DXF34).
GN DXF34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97419273; PubMed=9271673;
RA Laval S.H., Reed V., Blair H.J., Boyd Y.;
RT "The structure of DXF34, a human X-linked sequence family with
RT homology to a transcribed mouse Y-linked repeat.";
RL Mamm. Genome 8:689-691(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
```

CC -!- SIMILARITY: BELONGS TO THE SPIN / STSY FAMILY.  
CC -----  
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CC -----  
DR EMBL; Y09858; CAA70988.1; -  
DR EMBL; AL022157; CAA18148.1; -  
DR EMBL; AL022157; CAA18149.1; -  
DR InterPro; IPR003671; Spin\_Ssty.  
DR Pfam; PF02513; Spin\_Ssty; 3.  
KW Developmental protein; Phosphorylation; Cell cycle.  
FT MOD\_RES 196 196 PHOSPHORYLATION (POTENTIAL).  
FT MOD\_RES 224 224 PHOSPHORYLATION (POTENTIAL).  
FT MOD\_RES 20 20 C -> R (IN REF. 2).  
FT CONFLICT 208 208 T -> A (IN REF. 2; CAA18149).  
SQ SEQUENCE 232 AA; 26536 MW; 093E7B9F5340BF71 CRC64;  
  
Query Match 70.8%; Score 34; DB 1; Length 232;  
Best Local Similarity 75.0%; Pred. No. 17;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 QSSEDPPT 9  
: : : : :  
Db 165 ESSESPT 172  
  
RESULT 14  
GLHR ANTEL  
ID GLHR ANTEL STANDARD; PRT; 925 AA.  
AC P35409;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Probable glycoprotein hormone G-protein coupled receptor precursor.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
SQ SEQUENCE FROM N.A.  
RX MEDLINE=94107299; PubMed=8280121;  
RZ Nothacker H.-P.; Grimmelikhuijzen C.J.P.;  
RT "Molecular cloning of a novel, putative G protein-coupled receptor  
RT from sea anemones structurally related to members of the FSH, TSH,  
RL LH/CG receptor family from mammals."  
RL Biochem. Biophys. Res. Commun. 197;1062-1069(1993).  
CC -!- FUNCTION: PROBABLE RECEPTOR FOR A GLYCOPROTEIN HORMONE.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC FSH/LSH/TSH SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL; Z28332; CAA82186.1; -  
DR PIR; S41908; S41908.  
DR PIR; JC2033; JC2033.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR003592; LRR\_out.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR Pfam; PF00560; LRR; 6.

DR SMART; SM00370; LRR; 2.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP\_FL\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECP\_FL\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
KW Alternative splicing; Repeat.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 925 PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN  
FT COUPLED RECEPTOR.  
FT DOMAIN 28 529 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 530 551 1 (POTENTIAL).  
FT DOMAIN 552 561 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 562 584 2 (POTENTIAL).  
FT DOMAIN 585 606 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 607 628 3 (POTENTIAL).  
FT DOMAIN 629 651 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 652 673 4 (POTENTIAL).  
FT DOMAIN 674 691 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 692 712 5 (POTENTIAL).  
FT DOMAIN 713 739 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 740 763 6 (POTENTIAL).  
FT DOMAIN 764 774 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 775 795 7 (POTENTIAL).  
FT DOMAIN 796 925 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 333 461 5 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 333 349 1 (INCOMPLETE).  
FT REPEAT 350 384 2.  
FT REPEAT 385 419 3.  
FT REPEAT 420 453 4.  
FT REPEAT 454 461 5 (INCOMPLETE).  
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPPLIC 235 925 MISSING (IN SHORT ISOFORM).  
SQ SEQUENCE 925 AA; 100059 MW; D03A256368452FBD CRC64;  
  
Query Match 70.8%; Score 34; DB 1; Length 925;  
Best Local Similarity 75.0%; Pred. No. 80;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 QSSEDPPT 9  
: : : : :  
Db 478 QSTADPPT 485  
  
RESULT 15  
P531\_HUMAN  
ID P531\_HUMAN STANDARD; PRT; 1972 AA.  
AC Q12888;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor suppressor p53-binding protein 1 (p53-binding protein 1)  
DE (53BP1).  
DE GN TP53BP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SQ SEQUENCE FROM N.A. AND SUBCELLULAR LOCATION.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=98421532; PubMed=9748285;  
RT Iwabuchi K., Li B., Massa H.F., Trask B.J., Date T., Fields S.;  
RT "Stimulation of p53-mediated transcriptional activation by the  
RT p53-binding proteins, 53BP1 and 53BP2."  
RL J. Biol. Chem. 273:26061-26068(1998).  
RN [2]  
RN SEQUENCE OF 946-1972 FROM N.A.  
RX MEDLINE=94286584; PubMed=8016121;  
RA Iwabuchi K., Bartel P.L., Li B., Marraccino R., Fields S.;  
RT "Two cellular proteins that bind to wild-type but not mutant p53.";

```

RL  Proc. Natl. Acad. Sci. U.S.A. 91:6098-6102(1994).
CC  -!- FUNCTION: ENHANCES P53-MEDIATED TRANSCRIPTIONAL ACTIVATION.
CC  -!- SUBUNIT: BINDS TO THE CENTRAL DOMAIN OF P53.
CC  -!- SUBCELLULAR LOCATION: NUCLEAR. BOTH NUCLEAR AND CYTOPLASMIC
CC      IN SOME CELLS.
CC  -!- SIMILARITY: CONTAINS 2 BRCT DOMAINS.
CC  -----
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CC  -----
DR  EMBL; AF078776; AAC62018.1; -.
DR  EMBL; U09477; AAA21596.1; -.
DR  Genew; HGNC:11999; TP53BP1.
DR  MIM; 605230; -.
DR  InterPro; IPR001357; BRCT.
DR  SMART; SM00292; BRCT; 2.
DR  PROSITE; PS01172; BRCT; 2.
KW  Nuclear protein; Transcription regulation; Activator; Repeat.
FT  DOMAIN 1724 1848 BRCT 1.
FT  DOMAIN 1864 1964 BRCT 2.
FT  DOMAIN 1642 1646 POLY-SER.
FT  DOMAIN 1760 1764 POLY-GLU.
SQ  SEQUENCE 1972 AA; 213573 MW; 13E2CC8A265F9D2A CRC64;

Query Match      70.8%; Score 34; DB 1; Length 1972;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 SEDPPT 9
Db  1050 SEDPPT 1055

Search completed: February 14, 2003, 11:16:24
Job time : 5.64516 secs

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OM protein - protein search, using sw model

Run on: February 14, 2003, 11:10:17 ; Search time 18.7258 Seconds  
(without alignments)  
99.030 Million cell updates/sec

Title: US-09-701-001b-6  
Perfect score: 48  
Sequence: 1 QOSSEDPPT 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

ched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.rodent:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*
- 15: sp.virus:\*
- 16: sp.bacteriaph:\*
- 17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 38    | 79.2        | 301    | 10 Q9SN12 | Q9sn12 arabidopsis  |
| 2          | 38    | 79.2        | 304    | 10 Q49745 | Q49745 arabidopsis  |
| 3          | 38    | 79.2        | 304    | 10 Q39155 | Q39155 arabidopsis  |
| 4          | 38    | 79.2        | 564    | 11 Q9CTV2 | Q9ctv2 mus musculus |
| 5          | 37    | 77.1        | 442    | 10 Q82263 | Q82263 arabidopsis  |
| 6          | 35    | 72.9        | 265    | 10 Q8SA13 | Q8sa13 oryza sativ  |
| 7          | 35    | 72.9        | 231    | 5 Q8SUS0  | Q8sus0 oncephalito  |
| 8          | 35    | 72.9        | 305    | 10 Q9FDW1 | Q9fdw1 arabidopsis  |
| 9          | 35    | 72.9        | 305    | 10 Q941B3 | Q941b3 arabidopsis  |
| 10         | 35    | 72.9        | 479    | 4 Q15523  | Q15523 homo sapien  |
| 11         | 35    | 72.9        | 874    | 11 Q99J97 | Q99j97 mus musculus |
| 12         | 35    | 72.9        | 1068   | 5 Q9W3X2  | Q9w3x2 drosophila   |
| 13         | 35    | 72.9        | 1115   | 10 Q9C5K1 | Q9c5k1 arabidopsis  |
| 14         | 35    | 72.9        | 1116   | 10 Q9FPT1 | Q9fpt1 arabidopsis  |
| 15         | 35    | 72.9        | 1126   | 10 Q9FG10 | Q9fg10 arabidopsis  |
| 16         | 35    | 72.9        | 1716   | 11 Q99WS7 | Q99ws7 mus musculus |

Q9f293 yersinia en  
Q9har1 halobacteri  
Q9b8y0 trypanosoma  
Q9bpz2 homo sapien  
Q9sbf6 arabidopsis  
Q23160 arabidopsis  
Q9u8w4 eptaretus  
Q8z4j9 yersinia pe  
Q8t263 dictyosteli  
Q9bz18 homo sapien  
Q9hlj1 homo sapien  
Q9ffk3 arabidopsis  
Q85056 atkinsonell  
Q95z15 caenorhabdi  
Q23501 caenorhabdi  
Q43150 homo sapien  
Q9esv1 rattus norv  
Q8r4u7 mus musculu  
Q95va3 drosophila  
Q9v416 drosophila  
Q9w406 drosophila  
Q95va5 drosophila  
Q9vsk5 drosophila  
Q9nhx6 drosophila  
Q8t9n4 drosophila  
Q96jp6 homo sapien  
Q8wxq6 homo sapien  
Q96p79 homo sapien  
Q8v2a4 human herpe

## ALIGNMENTS

### RESULT 1

| ID | Q9SN12   | PRELIMINARY; | PRT; | 301 AA. |
|----|--|--------------|------|---------|
| AC | Q9SN12:  |              |      |         |
| DT | 01-MAY-2000 (Tremblrel. 13, Created)                                   |              |      |         |
| DT | 01-MAY-2000 (Tremblrel. 13, Last sequence update)                      |              |      |         |
| DT | 01-MAR-2002 (Tremblrel. 20, Last annotation update)                    |              |      |         |
| DE | R2R3-MYB transcription factor (AT3g50060/F3A4_140).                    |              |      |         |
| GN | F3A4.140.  |              |      |         |
| OS | Arabidopsis thaliana (Mouse-ear cross).                                |              |      |         |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;     |              |      |         |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  |              |      |         |
| OC | eurosid II; Brassicales; Brassicaceae; Arabidopsi                      |              |      |         |
| OX | NCBI_TaxID=3702;   |              |      |         |
| RN | [1]  |              |      |         |
| RP | SEQUENCE FROM N.A.   |              |      |         |
| RA | Bargues M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,       |              |      |         |
| RA | Newes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;        |              |      |         |
| RL | Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.                |              |      |         |
| RN | [2]  |              |      |         |
| RP | SEQUENCE FROM N.A.   |              |      |         |
| RA | EU Arabidopsis sequencing project;                                     |              |      |         |
| RL | Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.                |              |      |         |
| RN | [3]  |              |      |         |
| RP | SEQUENCE FROM N.A.   |              |      |         |
| RA | Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,         |              |      |         |
| RA | Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,     |              |      |         |
| RA | Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,         |              |      |         |
| RA | Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., |              |      |         |
| RA | Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., |              |      |         |
| RA | Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,     |              |      |         |
| RA | Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,     |              |      |         |
| RA | Ecker J.R.;  |              |      |         |
| RT | "Arabidopsis cDNA clones";   |              |      |         |
| RL | Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.                |              |      |         |
| CC | -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).                     |              |      |         |
| CC | -!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.                           |              |      |         |
| DR | EMBL; AL132978; CAB62114.1; -  |              |      |         |
| DR | EMBL; AF424588; AAL11582.1; -  |              |      |         |

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DR HSSP; P01103; IPOM.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA_binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS00090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 301 AA; 33111 MW; 9CDD5863E9D06DEC CRC64;

Query Match 79.2%; Score 38; DB 10; Length 301;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
Db 197 SSEDPT 203

RESULT 2
O49745 PRELIMINARY; PRT; 304 AA.
O49745;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE R2R3-MYB transcription factor.
GN ATWB77.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Romero I., Fuentes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;
RT "One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
DR EMBL; Y14208; CAA74604.1; -.
DR EMBL; Y14208; CAA74604.1; -.
DR HSSP; P01103; IPOM.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA_binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS00090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
VARIANT 136 136 S -> P.
VARIANT 298 298 I -> V.
SQ SEQUENCE 304 AA; 33296 MW; 53AE63F19CC24B42 CRC64;

Query Match 79.2%; Score 38; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
Db 197 SSEDPT 203

RESULT 3
ID Q39155 PRELIMINARY; PRT; 304 AA.
AC Q39155;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MYB-related protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LANDSBERG ERCTA; TISSUE=SILTIQUES;
RX MEDLINE=98341717; PubMed=9678577;
RA Kirik V., Kolle K., Misera S., Baumelein H.;
RT "Two novel MYB homologues with changed expression in late
RT embryogenesis-defective Arabidopsids mutants.";
RL Plant Mol. Biol. 37:819-827(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
DR EMBL; Z54137; CAA90810.1; -.
DR HSSP; P01103; IPOM.
DR TRANSFAC; T02590; -.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA_binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS00090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 304 AA; 33292 MW; EFA25289C3FD5A21 CRC64;

Query Match 79.2%; Score 38; DB 10; Length 304;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSEDPT 9
Db 197 SSEDPT 203

RESULT 4
ID Q9CTV2 PRELIMINARY; PRT; 564 AA.
AC Q9CTV2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 493434L15Rik protein (Fragment).
GN 493434L15Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=THYMUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guncich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK020021; BAB31969.1; -.
DR MGD; MGI:1914803; 493343L15Rik.
DR InterPro; IPR004046; GST_Cterm.
```

DR InterPro: IPR000051; SAM\_bind.  
 DR Pfam: PF0043; GST\_C; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 564 AA; 62710 MW; 8EAF7A27E35B53DA CRC64;

Query Match 79.2%; Score 38; DB 11; Length 564;  
 Best Local Similarity 77.8%; Pred. No. 19;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
 : : : : :  
 Db 94 QESSEHPPT 102

RESULT 5  
 O82263 PRELIMINARY; PRT; 442 AA.  
 ID O82263; Q944K4;

01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Expressed protein (A22947960/T923.10) (Hypothetical 49.3 kDa protein).  
 GN AT2947960.

OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,  
 RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Lin X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Town C.D., Kaul S.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [4]  
 RP SEQUENCE FROM N.A.  
 RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;

RT "Arabidopsis cDNA clones";  
 RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,  
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,  
 RA Davis R.W., Ecker J.R., Theologis A.;  
 RT "Full length cDNA of gene At2g47960 (GI:15227177).";  
 RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,

RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,  
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
 RA Fraser C.M., Venter J.C.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC005309; AAC63650.2; -;  
 DR EMBL; AF428334; AAL16264.1; -;  
 DR EMBL; AY074352; AAL67048.1; -;  
 DR EMBL; AC006072; AAM15133.1; -;  
 KW Hypothetical protein  
 SQ SEQUENCE 442 AA; 49290 MW; D6E987FA3D95BE30 CRC64;

Query Match 77.1%; Score 37; DB 10; Length 442;  
 Best Local Similarity 66.7%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 9  
 : : : : :  
 Db 246 EDSTEDPPT 254

RESULT 6  
 Q8SA13 PRELIMINARY; PRT; 265 AA.  
 ID Q8SA13

AC Q8SA13;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE P0703B11.5 protein.  
 GN P0703B11.5.

OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 clone:P0703B11.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP003302; BAB85286.1; -;  
 SQ SEQUENCE 265 AA; 29807 MW; C779784F75C06E7F CRC64;

Query Match 72.9%; Score 35; DB 10; Length 265;  
 Best Local Similarity 75.0%; Pred. No. 36;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSSEDPPT 8  
 : : : : :  
 Db 93 QHNSDDPP 100

RESULT 7  
 Q8SUS0 PRELIMINARY; PRT; 291 AA.  
 ID Q8SUS0;  
 AC Q8SUS0;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DE Hypothetical protein EC008\_0540.  
 GN EC008\_0540.

OS Encephalitozoon cuniculi.  
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.  
 OX NCBI\_TaxID=6035;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;  
 RA Genoscope;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GB-M1;

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RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590448; CAD26359.1; -.
KW Hypothetical protein.
SQ SEQUENCE 291 AA; 31902 MW; 70ABBA50CD45D35 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 291;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 8
Db 268 QNASDEPPT 275
PRT; 305 AA.
PRELIMINARY;
AC Q9FDW1;
ID Q9FDW1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative myb-related protein (Myb-related protein, 33.3K).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full Length cDNA of gene K8K14.2 (GI:9758429).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98162728; PubMed=9501987;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asanizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned pl clones.";
DNA Res. 4:401-414(1997).
[3]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Theologis A.;
RT "Full Length cDNA of gene K8K14.2 (GI:9758429).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
DR EMBL; AF326877; AAG41459.1; -.
DR EMBL; AB007645; BAB09015.1; -.
DR EMBL; AF339698; AAK00380.1; -.
DR HSP: P01103; 1POM.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.

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DR PROSITE; PS50090; MYB_3; 2.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 305 AA; 33268 MW; FDD31F9916E14D9D CRC64;

Query Match 72.9%; Score 35; DB 10; Length 305;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSEDPT 9
Db 186 SDDPPT 192
PRT; 305 AA.
PRELIMINARY;
AC Q941B3;
ID Q941B3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AT5g67300/K8K14.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052297; AAK96490.1; -.
DR EMBL; AY061923; AAL31250.1; -.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_2.
DR PROSITE; PS50090; MYB_3; 2.
SQ SEQUENCE 305 AA; 33282 MW; FDD31F990BDBE4F CRC64;

Query Match 72.9%; Score 35; DB 10; Length 305;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSEDPT 9
Db 186 SDDPPT 192
PRT; 479 AA.
PRELIMINARY;
ID Q15523;
AC Q15523;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

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Best Local Similarity 66.7%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSSEDPPT 9  
DB 114 QOSQPPPT 122

RESULT 13

Q9C5K1 PRELIMINARY; PRT; 1115 AA.  
AC Q9C5K1; (TREMREL. 17, Created)  
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)  
DT 01-JUN-2001 (TREMREL. 21, Last annotation update)  
DE Putative ubiquitin carboxyl-terminal hydrolase.  
GN F15M7.13/AT5G06600.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_TaxID=3702;

[1]

SEQUENCE FROM N.A.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,  
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,  
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,  
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,  
RA Theologis A.;  
RT "Full length cDNA of gene F15M7.13/AT5G06600 (GI:10178116).";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF360198; AAK25908.1; -  
DR InterPro; IPR002083; MATH.  
DR InterPro; IPR001394; UCH-2.  
DR InterPro; IPR000626; Ubiquitin.  
DR Pfam; PF00917; MATH; 1.  
DR Pfam; PF00240; ubiquitin; 1.  
DR Pfam; PF00442; UCH-1; 1.  
DR Pfam; PF00443; UCH-2; 1.  
DR SMART; SM00061; MATH; 1.  
DR PROSITE; PS00304; SASP\_1; UNKNOWN\_1.  
DR PROSITE; PS00972; UCH\_2\_1; 1.  
DR PROSITE; PS00973; UCH\_2\_2; 1.  
DR PROSITE; PS0235; UCH\_2\_3; 1.  
KW Hydrolase.

SEQUENCE 1115 AA; 130478 MW; 4AB4E10D836C2172 CRC64;

Query Match 72.9%; Score 35; DB 10; Length 1115;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QOSSEDPPT 9  
DB 46 QPAEDPPT 53

RESULT 14

Q9FP11 PRELIMINARY; PRT; 1116 AA.  
AC Q9FP11; (TREMREL. 16, Created)  
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)  
DE Ubiquitin-specific protease 12.  
GN UB12.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_TaxID=3702;

[1]  
SEQUENCE FROM N.A.

RA MEDLINE=20567829; PubMed=11115897;  
RA Yan N., Doelling J.H., Falbel T.G., Durski A.M., Vierstra R.D.;  
RT "The Ubiquitin-Specific Protease Family from Arabidopsis. AtUBP1 and 2  
Are Required for the Resistance to the Amino Acid Analog Canavanine.";  
RL Plant Physiol. 124:1828-1843(2000).  
DR EMBL; AF302663; AAG42754.1; -  
DR InterPro; IPR002083; MATH.  
DR InterPro; IPR001448; SASP.  
DR InterPro; IPR00626; Ubiquitin.  
DR InterPro; IPR001394; UCH-2.  
DR Pfam; PF00917; MATH; 1.  
DR Pfam; PF00240; ubiquitin; 1.  
DR Pfam; PF00442; UCH-1; 1.  
DR Pfam; PF00443; UCH-2; 1.  
DR SMART; SM00061; MATH; 1.  
DR PROSITE; PS00304; SASP\_1; UNKNOWN\_1.  
DR PROSITE; PS00972; UCH\_2\_1; 1.  
DR PROSITE; PS00973; UCH\_2\_2; 1.  
DR PROSITE; PS0235; UCH\_2\_3; 1.  
KW Protease.

SEQUENCE 1116 AA; 130640 MW; E5534164E5B66C88 CRC64;

Query Match 72.9%; Score 35; DB 10; Length 1116;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QOSSEDPPT 9  
DB 47 QPAEDPPT 54

RESULT 15

Q9FG10 PRELIMINARY; PRT; 1126 AA.  
AC Q9FG10; (TREMREL. 16, Created)  
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)  
DE Ubiquitin carboxyl-terminal hydrolase.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_TaxID=3702;

[1]  
SEQUENCE FROM N.A.

RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP002543; BAB11409.1; -  
DR InterPro; IPR002083; MATH.  
DR InterPro; IPR001448; SASP.  
DR InterPro; IPR00626; Ubiquitin.  
DR InterPro; IPR001394; UCH-2.  
DR Pfam; PF00917; MATH; 1.  
DR Pfam; PF00240; ubiquitin; 1.  
DR Pfam; PF00442; UCH-1; 1.  
DR Pfam; PF00443; UCH-2; 1.  
DR SMART; SM00061; MATH; 1.  
DR PROSITE; PS00304; SASP\_1; UNKNOWN\_1.  
DR PROSITE; PS00972; UCH\_2\_1; 1.  
DR PROSITE; PS00973; UCH\_2\_2; 1.  
DR PROSITE; PS0235; UCH\_2\_3; 1.  
KW Hydrolase.

SEQUENCE 1126 AA; 131869 MW; 2478F44417BF1768 CRC64;

Query Match 72.9%; Score 35; DB 10; Length 1126;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

us-09-701-001b-6.rspt

Fri Feb 14 15:01:00 2003

Qy 2 QSSDPPT 9  
| :|||||  
Db 56 QPAEDPPT 63

Search completed: February 14, 2003, 11:18:45  
Job time : 20.8925 secs

